

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Wild, Martha A.
Cochran, Mark D.
- (ii) TITLE OF INVENTION: RECOMBINANT INFECTIOUS LARYNGOTRACHEITIS VIRUS
AND USES THEREOF
- (iii) NUMBER OF SEQUENCES: 72
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Cooper & Dunham LLP
 - (B) STREET: 1185 Avenue of the Americas
 - (C) CITY: New York
 - (D) STATE: New York
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 10036
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE: 23-MAR-1995
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/126,597
 - (B) FILING DATE: 24-SEP-1993
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: White, John P.
 - (B) REGISTRATION NUMBER: 28,678
 - (C) REFERENCE/DOCKET NUMBER: 39116-A
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (212) 278-0400
 - (B) TELEFAX: (212) 391-0525

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13473 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1059..2489
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2575..4107

TOP SECRET 446660

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCCGTGCCCC	TAAAGGCCGC	CGAGAAAGCT	AAGTCCAAAT	GTGACGTCGG	AGGTCTCGAC	60
ATGGTCGCCA	ACCCCTCCAA	TGCTACCCGC	CGGCCCACGC	AACGCGGGCT	TTTATAAAGA	120
TGGCGCGCGA	GACAATAACA	CTTACTCATC	CGCGTACGCG	TTTATTATTG	TCAATATTTG	180
TGTGGTTATT	ATTACTGCTA	CCGCCCTTGT	TTCTGCAAGG	CCCTCGCCGC	GGCCCAGGCC	240
ACTATTCCGG	CAGCGGCCGC	CGACCGGGCG	AGCGTCGCCG	CTAACGTCGG	CGCCGCGGGG	300
AGCGGGGTTT	CTTCGACTTA	AATAGACTCC	CGAGAAAAAA	TTTTGGCTGC	CGTTCGCCAT	360
CATCCGAGTC	GGAAACACAG	TATGCGGCCG	AGTTAGGTTT	TACTTTTAAA	AACTTTACCG	420
TGCTGTACGG	CCAGGGCGTT	CTCAGGCTCG	AAGGGGCAAG	AGTTGTCCAG	ACTGATGGGT	480
GA CTCAGAGA	CAGCGTTGTC	TTGTCTCCGT	TTACCAAAAA	TATTTCCACT	CCTCTCTCAA	540
AATTTTTTACC	TCCGGTTTCG	GTAATTAGGA	AAGTTTTTTG	CGCAGGGAGG	TTTAAAGCTG	600
CCATGCATAT	GTCAGCGGTA	CCCAGCACCC	ACAAATGGAA	CTCTTTTGCG	GCATACGCGC	660
CAGATGACAA	ATGGTAAAAAC	CCTGCGTCCA	AGCCGCTCCA	CTCGGGACTT	ACTCCAGGCG	720
GGTCGCCCCC	CTCACCGAAC	CGAATCACGG	GTCTGCACAT	CCTGGGAAGG	GAAAACAGCT	780
CCCCGGAAAC	TTCGTACAGA	GATGCCGGGC	GCACGATTAC	CGATAATGTA	CTCGGACGAT	840
CGTAACTCGC	CATAGTTTTT	ACTGCGTGAA	CCAATTCTTT	CCATCCAGAA	TCCGAGAGCT	900
CAAATCTAGA	ATTAGGTAGT	TTGTAGTGCG	AATCGACCGC	AGAAACTATA	GTCACTTTTA	960
CAGGCGCCAT	CGCCGCTCAG	ACTCCACCCC	GCTATGATGT	CAGAAATATA	ACGCTCTTAT	1020
TCTAGCAGAG	TCAGGCCAAT	ATATACAGCT	TAGAGAAG	ATG CGG TTT CGG CGC		1073
				Met Arg Phe Arg Arg		
				1	5	
ATC TGT TCA CGC TCT AGG GCA GAA AAA CGA AGA AGA ACA ACC GAG AAT						1121
Ile Cys Ser Arg Ser Arg Ala Glu Lys Arg Arg Arg Thr Thr Glu Asn						
	10		15		20	

CCG	CTT	ACC	TCA	AAA	CGC	GTT	TGC	GTA	TTG	GAT	AGT	TTC	TCA	CGG	ACA	1169
Pro	Leu	Thr	Ser	Lys	Arg	Val	Cys	Val	Leu	Asp	Ser	Phe	Ser	Arg	Thr	
			25					30					35			
ATG	TCA	TTG	CGC	CCC	TAT	GCA	GAA	ATT	TTG	CCG	ACC	GCG	GAA	GGC	GTC	1217
Met	Ser	Leu	Arg	Pro	Tyr	Ala	Glu	Ile	Leu	Pro	Thr	Ala	Glu	Gly	Val	
		40					45					50				
GAG	CGC	CTC	GCC	GAA	CTT	GTT	AGT	GTG	ACA	ATG	ACA	GAA	CGC	GCG	GAA	1265
Glu	Arg	Leu	Ala	Glu	Leu	Val	Ser	Val	Thr	Met	Thr	Glu	Arg	Ala	Glu	
	55					60					65					
CCT	GTG	ACA	GAG	AAT	ACA	GCT	GTA	AAC	AGT	ATC	CCC	CCG	GCT	AAC	GAG	1313
Pro	Val	Thr	Glu	Asn	Thr	Ala	Val	Asn	Ser	Ile	Pro	Pro	Ala	Asn	Glu	
70					75					80					85	
AAC	GGG	CAG	AAC	TTC	GCA	TAT	GCA	GGC	GAT	GGG	CCC	TCG	ACT	ACT	GAA	1361
Asn	Gly	Gln	Asn	Phe	Ala	Tyr	Ala	Gly	Asp	Gly	Pro	Ser	Thr	Thr	Glu	
				90					95					100		
AAA	GTT	GAC	GGC	TCG	CAT	ACA	GAC	TTC	GAT	GAA	GCA	TCG	AGC	GAC	TAC	1409
Lys	Val	Asp	Gly	Ser	His	Thr	Asp	Phe	Asp	Glu	Ala	Ser	Ser	Asp	Tyr	
			105					110					115			
GCC	GGC	CCT	GTC	CCG	CTC	GCG	CAA	ACT	AGA	TTG	AAG	CAT	TCG	GAT	GAA	1457
Ala	Gly	Pro	Val	Pro	Leu	Ala	Gln	Thr	Arg	Leu	Lys	His	Ser	Asp	Glu	
		120					125					130				
TTT	CTT	CAG	CAC	TTC	CGA	GTT	TTA	GAC	GAT	TTG	GTG	GAG	GGG	GCT	TAC	1505
Phe	Leu	Gln	His	Phe	Arg	Val	Leu	Asp	Asp	Leu	Val	Glu	Gly	Ala	Tyr	
	135					140					145					
GGG	TTT	ATC	TGC	GGC	GTC	CGT	CGC	TAC	ACC	GAG	GAA	GAG	CAA	CGT	CGA	1553
Gly	Phe	Ile	Cys	Gly	Val	Arg	Arg	Tyr	Thr	Glu	Glu	Glu	Gln	Arg	Arg	
150					155					160					165	
AGA	GGG	GTT	AAC	AGT	ACT	AAC	CAG	GGG	AAA	TCA	AAA	TGT	AAG	CGC	CTG	1601
Arg	Gly	Val	Asn	Ser	Thr	Asn	Gln	Gly	Lys	Ser	Lys	Cys	Lys	Arg	Leu	
				170					175					180		
ATA	GCT	AAA	TAT	GTG	AAA	AAT	GGA	ACA	AGG	GCG	GCC	TCT	CAG	CTG	GAA	1649
Ile	Ala	Lys	Tyr	Val	Lys	Asn	Gly	Thr	Arg	Ala	Ala	Ser	Gln	Leu	Glu	
			185					190					195			
AAT	GAA	ATT	TTG	GTT	CTC	GGG	CGC	CTA	AAT	CAC	GAG	AAT	GTT	CTC	AAG	1697
Asn	Glu	Ile	Leu	Val	Leu	Gly	Arg	Leu	Asn	His	Glu	Asn	Val	Leu	Lys	
		200					205					210				
ATC	CAG	GAA	ATC	CTT	CGG	TAC	CCG	GAT	AAT	ACG	TAC	ATG	TTA	ACG	CAG	1745
Ile	Gln	Glu	Ile	Leu	Arg	Tyr	Pro	Asp	Asn	Thr	Tyr	Met	Leu	Thr	Gln	
	215					220					225					
AGG	TAT	CAG	TTC	GAC	TTG	TAC	AGC	TAC	ATG	TAC	GAT	GAA	GCG	TTC	GAC	1793
Arg	Tyr	Gln	Phe	Asp	Leu	Tyr	Ser	Tyr	Met	Tyr	Asp	Glu	Ala	Phe	Asp	
230					235					240					245	
TGG	AAA	GAC	AGT	CCA	ATG	CTT	AAA	CAG	ACT	AGA	CGC	ATC	ATG	AAG	CAG	1841
Trp	Lys	Asp	Ser	Pro	Met	Leu	Lys	Gln	Thr	Arg	Arg	Ile	Met	Lys	Gln	
				250					255					260		
CTC	ATG	TCA	GCG	GTC	TCG	TAT	ATC	CAT	TCA	AAG	AAA	CTG	ATT	CAC	AGG	1889
Leu	Met	Ser	Ala	Val	Ser	Tyr	Ile	His	Ser	Lys	Lys	Leu	Ile	His	Arg	
			265					270					275			
GAC	ATC	AAA	CTC	GAA	AAT	ATT	TTC	TTA	AAC	TGC	GAC	GGC	AAG	ACA	GTG	1937
Asp	Ile	Lys	Leu	Glu	Asn	Ile	Phe	Leu	Asn	Cys	Asp	Gly	Lys	Thr	Val	
		280					285					290				

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CTG GGC GAC TTT GGA ACT GTC ACG CCT TTT GAA AAT GAG CGG GAG CCC Leu Gly Asp Phe Gly Thr Val Thr Pro Phe Glu Asn Glu Arg Glu Pro 295 300 305	1985
TTC GAA TAT GGA TGG GTG GGG ACC GTG GCT ACT AAC TCT CCC GAG ATA Phe Glu Tyr Gly Trp Val Gly Thr Val Ala Thr Asn Ser Pro Glu Ile 310 315 320 325	2033
CTC GCC AGG GAT TCG TAC TGT GAA ATT ACA GAC ATT TGG AGC TGC GGA Leu Ala Arg Asp Ser Tyr Cys Glu Ile Thr Asp Ile Trp Ser Cys Gly 330 335 340	2081
GTA GTA TTG CTG GAA ATG GTA AGC CAT GAA TTT TGC CCG ATC GGC GAT Val Val Leu Leu Glu Met Val Ser His Glu Phe Cys Pro Ile Gly Asp 345 350 355	2129
GGC GGG GGA AAT CCG CAC CAG CAA TTG CTG AAA GTT ATC GAC TCT CTC Gly Gly Gly Asn Pro His Gln Gln Leu Leu Lys Val Ile Asp Ser Leu 360 365 370	2177
TCA GTT TGT GAT GAA GAG TTC CCA GAC CCC CCG TGT AAT CTG TAC AAT Ser Val Cys Asp Glu Glu Phe Pro Asp Pro Pro Cys Asn Leu Tyr Asn 375 380 385	2225
TAT TTG CAT TAT GCG AGC ATC GAT CGC GCC GGA CAT ACG GTC CCG TCG Tyr Leu His Tyr Ala Ser Ile Asp Arg Ala Gly His Thr Val Pro Ser 390 395 400 405	2273
CTC ATA CGG AAC CTC CAC CTT CCG GCG GAT GTG GAA TAC CCT CTA GTT Leu Ile Arg Asn Leu His Leu Pro Ala Asp Val Glu Tyr Pro Leu Val 410 415 420	2321
AAA ATG CTT ACT TTT GAC TGG CGT TTG AGA CCC AGC GCG GCC GAA GTA Lys Met Leu Thr Phe Asp Trp Arg Leu Arg Pro Ser Ala Ala Glu Val 425 430 435	2369
TTG GCA ATG CCA CTG TTT TCG GCT GAA GAG GAA CGG ACC ATA ACA ATT Leu Ala Met Pro Leu Phe Ser Ala Glu Glu Glu Arg Thr Ile Thr Ile 440 445 450	2417
ATT CAT GGA AAA CAT AAA CCC ATC CGA CCC GAA ATC CGT GCG CGG GTG Ile His Gly Lys His Lys Pro Ile Arg Pro Glu Ile Arg Ala Arg Val 455 460 465	2465
CCA CGG TCC ATG AGT GAA GGT TAATAATAAAA GGACGGAGAT AGAGAACTGA Pro Arg Ser Met Ser Glu Gly 470 475	2516
AGCGTCAGAT TTTTTTAAAA AAATAAATGA TCGAGAACTT ATGATTTGTC TTTCTTGA	2574
ATG ACC TTG CCC CAT CGA TTA ACG AAA AGA CCT TTC GCG CGT CGA TTC Met Thr Leu Pro His Arg Leu Thr Lys Arg Pro Phe Ala Arg Arg Phe 1 5 10 15	2622
TGC TCG GTC TTT GTG ATA CAT TAT AGT GAG ACT AAA CTC GAC CGA TAT Cys Ser Val Phe Val Ile His Tyr Ser Glu Thr Lys Leu Asp Arg Tyr 20 25 30	2670
AAC AAG ACA ATG TTA CTC TAT AGA CCG GAC TCA ACC ATG CGG CAT AGC Asn Lys Thr Met Leu Leu Tyr Arg Pro Asp Ser Thr Met Arg His Ser 35 40 45	2718
GGA GGC GAC GCA AAT CAC AGA GGG ATA AGG CCG AGG CGG AAA TCT ATT Gly Gly Asp Ala Asn His Arg Gly Ile Arg Pro Arg Arg Lys Ser Ile 50 55 60	2766

TCGAGT " 22E5550

GGA GCG TTT AGC GCG CGC GAA AAG ACT GGA AAA CGA AAT GCG CTG ACG Gly Ala Phe Ser Ala Arg Glu Lys Thr Gly Lys Arg Asn Ala Leu Thr 65 70 75 80	2814
GAA AGC AGC TCC TCC TCC GAC ATG CTA GAT CCG TTT TCC ACG GAT AAG Glu Ser Ser Ser Ser Ser Asp Met Leu Asp Pro Phe Ser Thr Asp Lys 85 90 95	2862
GAA TTT GGC GGT AAG TGG ACG GTA GAC GGA CCT GCC GAC ATT ACT GCC Glu Phe Gly Gly Lys Trp Thr Val Asp Gly Pro Ala Asp Ile Thr Ala 100 105 110	2910
GAG GTC CTT TCT CAG GCA TGG GAC GTT CTC CAA TTA GTG AAG CAT GAA Glu Val Leu Ser Gln Ala Trp Asp Val Leu Gln Leu Val Lys His Glu 115 120 125	2958
GAT GCG GAG GAG GAG AGA GTG ACT TAT GAG TCC AAA CCG ACC CCG ATA Asp Ala Glu Glu Glu Arg Val Thr Tyr Glu Ser Lys Pro Thr Pro Ile 130 135 140	3006
CAG CCG TTC AAT GCC TGG CCG GAC GGG CCG AGT TGG AAC GCG CAG GAT Gln Pro Phe Asn Ala Trp Pro Asp Gly Pro Ser Trp Asn Ala Gln Asp 145 150 155 160	3054
TTT ACT CGA GCG CCA ATA GTT TAT CCC TCT GCG GAG GTA TTG GAC GCA Phe Thr Arg Ala Pro Ile Val Tyr Pro Ser Ala Glu Val Leu Asp Ala 165 170 175	3102
GAG GCG TTG AAA GTA GGG GCA TTC GTT AGC CGA GTT TTA CAA TGT GTA Glu Ala Leu Lys Val Gly Ala Phe Val Ser Arg Val Leu Gln Cys Val 180 185 190	3150
CCG TTC ACG CGA TCA AAG AAA AGC GTT ACG GTG CGG GAT GCG CAG TCG Pro Phe Thr Arg Ser Lys Lys Ser Val Thr Val Arg Asp Ala Gln Ser 195 200 205	3198
TTT TTG GGG GAC TCG TTC TGG AGA ATA ATG CAG AAC GTT TAC ACG GTT Phe Leu Gly Asp Ser Phe Trp Arg Ile Met Gln Asn Val Tyr Thr Val 210 215 220	3246
TGC TTA CGA CAG CAC ATA ACT CGA CTC AGG CAC CCT TCC AGC AAA AGC Cys Leu Arg Gln His Ile Thr Arg Leu Arg His Pro Ser Ser Lys Ser 225 230 235 240	3294
ATT GTT AAC TGC AAC GAC CCT CTA TGG TAC GCC TAC GCG AAT CAA TTT Ile Val Asn Cys Asn Asp Pro Leu Trp Tyr Ala Tyr Ala Asn Gln Phe 245 250 255	3342
CAC TGG AGA GGA ATG CGC GTG CCG TCG CTT AAA TTA GCC TCT CCC CCG His Trp Arg Gly Met Arg Val Pro Ser Leu Lys Leu Ala Ser Pro Pro 260 265 270	3390
GAG GAG AAT ATT CAA CAC GGC CCA ATG GCC GCC GTT TTT AGA AAC GCG Glu Glu Asn Ile Gln His Gly Pro Met Ala Ala Val Phe Arg Asn Ala 275 280 285	3438
GGG GCT GGT CTG TTC CTG TGG CCT GCC ATG CGC GCA GCC TTT GAA GAG Gly Ala Gly Leu Phe Leu Trp Pro Ala Met Arg Ala Phe Glu Glu 290 295 300	3486
CGC GAC AAG CGA CTG TTA AGA GCA TGC CTG TCT TCA CTC GAT ATC ATG Arg Asp Lys Arg Leu Leu Arg Ala Cys Leu Ser Ser Leu Asp Ile Met 305 310 315 320	3534
GAC GCA GCC GTC CTC GCG TCG TTT CCA TTT TAC TGG CGC GGC GTC CAA Asp Ala Ala Val Leu Ala Ser Phe Pro Phe Tyr Trp Arg Gly Val Gln 325 330 335	3582

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GAC Asp	ACC Thr	TCG Ser	CGC Arg 340	TTC Phe	GAG Glu	CCT Pro	GCG Ala	CTG Leu 345	GGC Gly	TGT Cys	TTG Leu	TCA Ser	GAG Glu 350	TAC Tyr	TTT Phe	3630
GCA Ala	CTA Leu	GTG Val 355	GTG Val	TTA Leu	CTG Leu	GCC Ala	GAG Glu 360	ACG Thr	GTC Val	TTA Leu	GCG Ala	ACC Thr 365	ATG Met	TTC Phe	GAC Asp	3678
CAC His	GCA Ala 370	CTG Leu	GTA Val	TTC Phe	ATG Met	AGG Arg 375	GCG Ala	CTG Leu	GCA Ala	GAC Asp	GGC Gly 380	AAT Asn	TTC Phe	GAT Asp	GAC Asp	3726
TAT Tyr 385	GAC Asp	GAA Glu	ACT Thr	AGA Arg	TAT Tyr 390	ATA Ile	GAC Asp	CCC Pro	GTT Val	AAA Lys 395	AAC Asn	GAG Glu	TAC Tyr	CTG Leu	AAC Asn 400	3774
GGA Gly	GCC Ala	GAG Glu	GGT Gly	ACT Thr 405	CTG Leu	TTA Leu	CGG Arg	GGC Gly	ATA Ile 410	GTG Val	GCC Ala	TCC Ser	AAC Asn	ACC Thr 415	GCT Ala	3822
CTG Leu	GCG Ala	GTG Val	GTT Val 420	TGC Cys	GCA Ala	AAC Asn	ACC Thr	TAT Tyr 425	TCG Ser	ACG Thr	ATA Ile	AGA Arg	AAA Lys 430	CTC Leu	CCG Pro	3870
TCC Ser	GTG Val 435	GCA Ala	ACT Thr	AGC Ser	GCG Ala	TGC Cys	AAT Asn 440	GTT Val	GCC Ala	TAC Tyr	AGG Arg	ACC Thr 445	GAA Glu	ACG Thr	CTG Leu	3918
AAA Lys 450	GCG Ala	AGG Arg	CGC Arg	CCT Pro	GGC Gly	ATG Met 455	AGC Ser	GAC Asp	ATA Ile	TAC Tyr	CGG Arg 460	ATA Ile	TTA Leu	CAA Gln	AAA Lys	3966
GAG Glu 465	TTT Phe	TTC Phe	TTT Phe	TAC Tyr 470	ATT Ile	GCG Ala	TGG Trp	CTC Leu	CAG Gln	AGG Arg 475	GTT Val	GCA Ala	ACA Thr	CAC His	GCA Ala 480	4014
AAT Asn	TTC Phe	TGT Cys	TTA Leu	AAC Asn 485	ATT Ile	CTG Leu	AAG Lys	AGA Arg	AGC Ser 490	GTG Val	GAT Asp	ACG Thr	GGC Gly	CCC Pro 495	CGC Arg	4062
CAT His	TTT Phe	TGT Cys	TCA Ser 500	GGG Gly	CCA Pro	GCT Ala	CGG Arg	AGA Arg 505	AGC Ser	GGC Gly	TGC Cys	AGC Ser	AGT Ser 510	TAAATAAA		4112
ATG Met 1	CTC Leu	TGC Cys	CCC Pro	CTT Leu 5	CTC Leu	GTG Val	CCG Pro	ATT Ile 10	CAA Gln	TAT Tyr	GAA Glu	GAC Asp	TTT Phe	TCG Ser 15	AAG Lys	4160
GCC Ala	ATG Met	GGG Gly	TCT Ser 20	GAG Glu	CTC Leu	AAG Lys	AGG Arg	GAA Glu 25	AAG Lys	TTA Leu	GAG Glu	ACA Thr 30	TTC Phe	GTT Val	AAA Lys	4208
GCT Ala	ATT Ile	TCC Ser 35	AGC Ser	GAC Asp	AGG Arg	GAC Asp	CCG Pro 40	AGG Arg	GGG Gly	TCC Ser	TTA Leu	AGA Arg 45	TTT Phe	CTC Leu	ATT Ile	4256
TCG Ser	GAC Asp 50	CAT His	GCA Ala	AGG Arg	GAA Glu	ATT Ile 55	ATT Ile	GCA Ala	GAC Asp	GGA Gly	GTA Val 60	CGG Arg	TTT Phe	AAG Lys	CCG Pro	4304
GTG Val 65	ATA Ile	GAC Asp	GAG Glu	CCG Pro 70	GTT Val	CGG Arg	GCT Ala	TCA Ser	GTT Val	GCG Ala 75	CTG Leu	AGT Ser	ACC Thr	GCT Ala 80	GCC Ala	4352
GCT Ala	GGG Gly	AAA Lys	GTG Val 85	AAA Lys	GCG Ala	CGA Arg	CGC Arg	TTA Leu 90	ACC Thr	TCA Ser	GTT Val	CGC Arg	GCG Ala 95	CCC Pro	GTA Val	4400

CCG CCC GCA GGC GCC GTT TCC GCG CGC CGG AAA TCG GAA ATA TGA TA	4447
Pro Pro Ala Gly Ala Val Ser Ala Arg Arg Lys Ser Glu Ile *	
100 105 110	
AAAATGCTTG GCATTTCGGG GCGAAGAGGC GTGATCTGAA GGGCTCCACA ATGACGTAAC	4507
TGAGCTACGC ATCCCTATAA AGTGTACSCG CTGACCGCTA GCCCATAACAG TGTTACAGGA	4567
GGGGAGAGAG ACAACTTCAG CTCGAAGTCT GAAGAGACAT C ATG AGC GGC	4617
Met Ser Gly	
1	
TTC AGT AAC ATA GGA TCG ATT GCC ACC GTT TCC CTA GTA TGC TCG CTT	4665
Phe Ser Asn Ile Gly Ser Ile Ala Thr Val Ser Leu Val Cys Ser Leu	
5 10 15	
TTG TGC GCA TCT GTA TTA GGG GCG CCG GTA CTG GAC GGG CTC GAG TCG	4713
Leu Cys Ala Ser Val Leu Gly Ala Pro Val Leu Asp Gly Leu Glu Ser	
20 25 30 35	
AGC CCT TTC CCG TTC GGG GGC AAA ATT ATA GCC CAG GCG TGC AAC CGC	4761
Ser Pro Phe Pro Phe Gly Gly Lys Ile Ile Ala Gln Ala Cys Asn Arg	
40 45 50	
ACC ACG ATT GAG GTG ACG GTC CCG TGG AGC GAC TAC TCT GGT CGC ACC	4809
Thr Thr Ile Glu Val Thr Val Pro Trp Ser Asp Tyr Ser Gly Arg Thr	
55 60 65	
GAA GGA GTG TCA GTC GAG GTG AAA TGG TTC TAC GGG AAT AGT AAT CCC	4857
Glu Gly Val Ser Val Glu Val Lys Trp Phe Tyr Gly Asn Ser Asn Pro	
70 75 80	
GAA AGC TTC GTG TTC GGG GTG GAT AGC GAA ACG GGC AGT GGA CAC GAG	4905
Glu Ser Phe Val Phe Gly Val Asp Ser Glu Thr Gly Ser Gly His Glu	
85 90 95	
GAC CTG TCT ACG TGC TGG GCT CTA ATC CAT AAT CTG AAC GCG TCT GTG	4953
Asp Leu Ser Thr Cys Trp Ala Leu Ile His Asn Leu Asn Ala Ser Val	
100 105 110 115	
TGC AGG GCG TCT GAC GCC GGG ATA CCT GAT TTC GAC AAG CAG TGC GAA	5001
Cys Arg Ala Ser Asp Ala Gly Ile Pro Asp Phe Asp Lys Gln Cys Glu	
120 125 130	
AAA GTG CAG AGA AGA CTG CGC TCC GGG GTG GAA CTT GGT AGT TAC GTG	5049
Lys Val Gln Arg Arg Leu Arg Ser Gly Val Glu Leu Gly Ser Tyr Val	
135 140 145	
TCT GGC AAT GGA TCC CTG GTG CTG TAC CCA GGG ATG TAC GAT GCC GGC	5097
Ser Gly Asn Gly Ser Leu Val Leu Tyr Pro Gly Met Tyr Asp Ala Gly	
150 155 160	
ATC TAC GCC TAC CAG CTC TCA GTG GGT GGG AAG GGA TAT ACC GGG TCT	5145
Ile Tyr Ala Tyr Gln Leu Ser Val Gly Gly Lys Gly Tyr Thr Gly Ser	
165 170 175	
GTT TAT CTA GAC GTC GGA CCA AAC CCC GGA TGC CAC GAC CAG TAT GGG	5193
Val Tyr Leu Asp Val Gly Pro Asn Pro Gly Cys His Asp Gln Tyr Ser	
180 185 190 195	
TAC ACC TAT TAC AGC CTG GCC GAC GAG GCG TCA GAC TTA TCA TCT TAT	5241
Tyr Thr Tyr Tyr Ser Leu Ala Asp Glu Ala Ser Asp Leu Ser Ser Tyr	
200 205 210	
GAC GTA GCC TCG CCC GAA CTC GAC GGT CCT ATG GAG GAA GAT TAT TCC	5289
Asp Val Ala Ser Pro Glu Leu Asp Gly Pro Met Glu Glu Asp Tyr Ser	
215 220 225	

AAT TGT CTA GAC ATG CCC CCG CTA CGC CCA TGG ACA ACC GTT TGT TCG	5337
Asn Cys Leu Asp Met Pro Pro Leu Arg Pro Trp Thr Thr Val Cys Ser	
230 235 240	
CAT GAC GTC GAG GAG CAG GAA AAC GCC ACG GAC GAG CTT TAC CTA TGG	5385
His Asp Val Glu Glu Gln Glu Asn Ala Thr Asp Glu Leu Tyr Leu Trp	
245 250 255	
GAC GAG GAA TGC GCC GGT CCG CTG GAC GAG TAC GTC GAC GAA AGG TCA	5433
Asp Glu Glu Cys Ala Gly Pro Leu Asp Glu Tyr Val Asp Glu Arg Ser	
260 265 270 275	
GAG ACG ATG CCC AGG ATG GTT GTC TTT TCA CCG CCC TCT ACG CTC CAG	5481
Glu Thr Met Pro Arg Met Val Val Phe Ser Pro Pro Ser Thr Leu Gln	
280 285 290	
CAG TAGCCACCCG AGAGTGT TTTT TTGTGAGCGC CCACGCAACA TACCTAACTG	5534
Gln	
CTTCATTTCT GATCAATTAT TGC GTATTGA ATAAATAAAC AGTACAAAAG CATCAGGTGT	5594
GGTTTGC GTG TCTGTGCTAA ACCATGGCGT GTGCGGGTGA AACCGTAAAT TACGTGATAA	5654
TAAATAGCAT AGGAGTTGGC GTGCAGCGTA TTTCGCCGAG AG ATG GGG ACA ATG	5708
Met Gly Thr Met	
1	
TTA GTG TTG CGC CTT TTC CTA CTT GCA GTA GCG GAC GCG GCG TTG CCG	5756
Leu Val Leu Arg Leu Phe Leu Leu Ala Val Ala Asp Ala Ala Leu Pro	
5 10 15 20	
ACC GGC AGA TTC TGC CGA GTT TGG AAG GTG CCT CCG GGA GGA ACC ATC	5804
Thr Gly Arg Phe Cys Arg Val Trp Lys Val Pro Pro Gly Gly Thr Ile	
25 30 35	
CAA GAG AAC CTG GCG GTG CTC GCG GAA TCG CCG GTC ACG GGA CAC GCG	5852
Gln Glu Asn Leu Ala Val Leu Ala Glu Ser Pro Val Thr Gly His Ala	
40 45 50	
ACA TAT CCG CCG CCT GAA GGC GCC GTC AGC TTT CAG ATT TTT GCG GAC	5900
Thr Tyr Pro Pro Pro Glu Gly Ala Val Ser Phe Gln Ile Phe Ala Asp	
55 60 65	
ACC CCT ACT TTG CGC ATT CGC TAC GGG CCT ACG GAG GAC GAA CTT GCA	5948
Thr Pro Thr Leu Arg Ile Arg Tyr Gly Pro Thr Glu Asp Glu Leu Ala	
70 75 80	
CTG GAG CGC GGG ACG TCC GCC TCA GAC GCG GAC AAC GTG ACA TTT TCG	5996
Leu Glu Arg Gly Thr Ser Ala Ser Asp Ala Asp Asn Val Thr Phe Ser	
85 90 95 100	
CTG TCA TAT CGC CCG CGC CCA GAA ATT CAC GGA GCA TAC TTC ACC ATA	6044
Leu Ser Tyr Arg Pro Arg Pro Glu Ile His Gly Ala Tyr Phe Thr Ile	
105 110 115	
GGG GTA TTC GCT ACT GGC CAG AGC ACG GAA AGC AGC TAT TCG GTC ATC	6092
Gly Val Phe Ala Thr Gly Gln Ser Thr Glu Ser Ser Tyr Ser Val Ile	
120 125 130	
AGT CGG GTC TTA GTT AAC GCC TCT CTG GAA CGG TCC GTG CGC CTG GAA	6140
Ser Arg Val Leu Val Asn Ala Ser Leu Glu Arg Ser Val Arg Leu Glu	
135 140 145	
ACG CCG TGC GAT GAA AAT TTT TTG CAG AAC GAG CCT ACA TGG GGC TCG	6188
Thr Pro Cys Asp Glu Asn Phe Leu Gln Asn Glu Pro Thr Trp Gly Ser	
150 155 160	

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AAG CGT TGG TTA GGC CCC CCG TCG CCT TAT GTG CGA GAT AAC GAT GTC Lys Arg Trp Leu Gly Pro Pro Ser Pro Tyr Val Arg Asp Asn Asp Val 165 170 175 180	6236
GCC GTG TTG ACA AAA GCG CAG TAC ATT GGG GAG TGC TAC TCC AAC TCG Ala Val Leu Thr Lys Ala Gln Tyr Ile Gly Glu Cys Tyr Ser Asn Ser 185 190 195	6284
GCG GCC CAG ACG GGG CTC ACG TCT CTC AAC ATG ACC TTT TTC TAT TCG Ala Ala Gln Thr Gly Leu Thr Ser Leu Asn Met Thr Phe Phe Tyr Ser 200 205 210	6332
CCT AAA AGA ATA GTA AAC GTC ACG TGG ACA ACC GGC GGC CCC TCC CCC Pro Lys Arg Ile Val Asn Val Thr Trp Thr Thr Gly Gly Pro Ser Pro 215 220 225	6380
TCG CGC ATA ACG GTA TAC TCG TCG CGG GAG AAC GGG CAG CCC GTG TTG Ser Arg Ile Thr Val Tyr Ser Ser Arg Glu Asn Gly Gln Pro Val Leu 230 235 240	6428
AGG AAC GTT TCT GAC GGG TTC TTG GTT AAG TAC ACT CCC GAC ATT GAC Arg Asn Val Ser Asp Gly Phe Leu Val Lys Tyr Thr Pro Asp Ile Asp 245 250 255 260	6476
GGC CGG GCC ATG ATA AAC GTT ATT GCC AAT TAT TCG CCG GCG GAC TCC Gly Arg Ala Met Ile Asn Val Ile Ala Asn Tyr Ser Pro Ala Asp Ser 265 270 275	6524
GGC AGC GTC CTC GCG TTT ACG GCC TTT AGG GAA GGA AAA CTC CCA TCC Gly Ser Val Leu Ala Phe Thr Ala Phe Arg Glu Gly Lys Leu Pro Ser 280 285 290	6572
GCG ATT CAA CTG CAC CGG ATA GAT ATG TCC GGG ACT GAG CCG CCG GGG Ala Ile Gln Leu His Arg Ile Asp Met Ser Gly Thr Glu Pro Pro Gly 295 300 305	6620
ACT GAA ACG ACC TTC GAC TGT CAA AAA ATG ATA GAA ACC CCG TAC CGA Thr Glu Thr Thr Phe Asp Cys Gln Lys Met Ile Glu Thr Pro Tyr Arg 310 315 320	6668
GCG CTC GGG AGC AAT GTT CCC AGG GAC GAC TCT ATC CGT CCG GGG GCC Ala Leu Gly Ser Asn Val Pro Arg Asp Asp Ser Ile Arg Pro Gly Ala 325 330 335 340	6716
ACT CTG CCT CCG TTC GAT ACC GCA GCA CCT GAT TTC GAT ACA GGT ACT Thr Leu Pro Pro Phe Asp Thr Ala Ala Pro Asp Phe Asp Thr Gly Thr 345 350 355	6764
TCC CCG ACC CCC ACT ACC GTG CCA GAG CCA GCC ATT ACT ACA CTC ATA Ser Pro Thr Pro Thr Thr Val Pro Glu Pro Ala Ile Thr Thr Leu Ile 360 365 370	6812
CCG CGC AGC ACT AGC GAT ATG GGA TTC TTC TCC ACG GCA CGT GCT ACC Pro Arg Ser Thr Ser Asp Met Gly Phe Phe Ser Thr Ala Arg Ala Thr 375 380 385	6860
GGA TCA GAA ACT CTT TCG GTA CCC GTC CAG GAA ACG GAT AGA ACT CTT Gly Ser Glu Thr Leu Ser Val Pro Val Gln Glu Thr Asp Arg Thr Leu 390 395 400	6908
TCG ACA ACT CCT CTT ACC CTT CCA CTG ACT CCC GGT GAG TCA GAA AAT Ser Thr Thr Pro Leu Leu Pro Leu Thr Pro Gly Glu Ser Glu Asn 405 410 415 420	6956
ACA CTG TTT CCT ACG ACC GCG CCG GGG ATT TCT ACC GAG ACC CCG AGC Thr Leu Phe Pro Thr Thr Ala Pro Gly Ile Ser Thr Glu Thr Pro Ser 425 430 435	7004

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GCG GCA CAT GAA ACT ACA CAG ACC CAG AGT GCA GAA ACG GTG GTC TTT Ala Ala His Glu Thr Thr Gln Thr Gln Ser Ala Glu Thr Val Val Phe 440 445 450	7052
ACT CAG AGT CCG AGT ACC GAG TCG GAA ACC GCG CGG TCC CAG AGT CAG Thr Gln Ser Pro Ser Thr Glu Ser Glu Thr Ala Arg Ser Gln Ser Gln 455 460 465	7100
GAA CCG TGG TAT TTT ACT CAG ACT CCG AGT ACT GAA CAG GCG GCT CTT Glu Pro Trp Tyr Phe Thr Gln Thr Pro Ser Thr Glu Gln Ala Ala Leu 470 475 480	7148
ACT CAG ACG CAG ATC GCA GAA ACG GAG GCG TTG TTT ACT CAG ACT CCG Thr Gln Thr Gln Ile Ala Glu Thr Glu Ala Leu Phe Thr Gln Thr Pro 485 490 495 500	7196
AGT GCT GAA CAG ATG ACT TTT ACT CAG ACT CCG GGT GCA GAA ACC GAG Ser Ala Glu Gln Met Thr Phe Thr Gln Thr Pro Gly Ala Glu Thr Glu 505 510 515	7244
GCA CCT GCC CAG ACC CCG AGC ACG ATA CCC GAG ATA TTT ACT CAG TCT Ala Pro Ala Gln Thr Pro Ser Thr Ile Pro Glu Ile Phe Thr Gln Ser 520 525 530	7292
CGT AGC ACG CCC CCC GAA ACC GCT CGC GCT CCG AGC GCG GCG CCG GAG Arg Ser Thr Pro Pro Glu Thr Ala Arg Ala Pro Ser Ala Ala Pro Glu 535 540 545	7340
GTT TTT ACA CAG AGT TCG AGT ACG GTA ACG GAG GTG TTT ACT CAG ACC Val Phe Thr Gln Ser Ser Thr Val Thr Glu Val Phe Thr Gln Thr 550 555 560	7388
CCG AGC ACG GTA CCG AAA ACT ACT CTG AGT TCG AGT ACT GAA CCG GCG Pro Ser Thr Val Pro Lys Thr Thr Leu Ser Ser Ser Thr Glu Pro Ala 565 570 575 580	7436
ATT TTT ACT CGG ACT CAG AGC GCG GGA ACT GAG GCC TTT ACT CAG ACT Ile Phe Thr Arg Thr Gln Ser Ala Gly Thr Glu Ala Phe Thr Gln Thr 585 590 595	7484
TCG AGT GCC GAG CCG GAC ACT ATG CGA ACT CAG AGT ACT GAA ACA CAC Ser Ser Ala Glu Pro Asp Thr Met Arg Thr Gln Ser Thr Glu Thr His 600 605 610	7532
TTT TTC ACT CAG GCC CCG AGT ACG GTA CCG AAA GCT ACT CAG ACT CCG Phe Phe Thr Gln Ala Pro Ser Thr Val Pro Lys Ala Thr Gln Thr Pro 615 620 625	7580
AGT ACA GAG CCG GAG GTG TTG ACT CAG AGT CCG AGT ACC GAA CCT GTG Ser Thr Glu Pro Glu Val Leu Thr Gln Ser Pro Ser Thr Glu Pro Val 630 635 640	7628
CCT TTC ACC CGG ACT CTG GGC GCA GAG CCG GAA ATT ACT CAG ACC CCG Pro Phe Thr Arg Thr Leu Gly Ala Glu Pro Glu Ile Thr Gln Thr Pro 645 650 655 660	7676
AGC GCG GCA CCG GAG GTT TAT ACT CGG AGT TCG AGT ACG ATG CCA GAA Ser Ala Ala Pro Glu Val Tyr Thr Arg Ser Ser Ser Thr Met Pro Glu 665 670 675	7724
ACT GCA CAG AGC ACA CCC CTG GCC TCG CAA AAC CCT ACC AGT TCG GGA Thr Ala Gln Ser Thr Pro Leu Ala Ser Gln Asn Pro Thr Ser Ser Gly 680 685 690	7772
ACC GGG ACG CAT AAT ACT GAA CCG AGG ACT TAT CCA GTG CAA ACG ACA Thr Gly His Asn Thr Glu Pro Arg Thr Tyr Pro Val Gln Thr Thr 695 700 705	7820

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CCA CAT ACC CAG AAA CTC TAC ACA GAA AAT AAG ACT TTA TCG TTT CCT	7868
Pro His Thr Gln Lys Leu Tyr Thr Glu Asn Lys Thr Leu Ser Phe Pro	
710 715 720	
ACT GTT GTT TCA GAA TTC CAT GAG ATG TCG ACG GCA GAG TCG CAG ACG	7916
Thr Val Val Ser Glu Phe His Glu Met Ser Thr Ala Glu Ser Gln Thr	
725 730 735 740	
CCC CTA TTG GAC GTC AAA ATT GTA GAG GTG AAG TTT TCA AAC GAT GGC	7964
Pro Leu Leu Asp Val Lys Ile Val Glu Val Lys Phe Ser Asn Asp Gly	
745 750 755	
GAA GTA ACG GCG ACT TGC GTT TCC ACC GTC AAA TCT CCC TAT AGG GTA	8012
Glu Val Thr Ala Thr Cys Val Ser Thr Val Lys Ser Pro Tyr Arg Val	
760 765 770	
GAA ACT AAT TGG AAA GTA GAC CTC GTA GAT GTA ATG GAT GAA ATT TCT	8060
Glu Thr Asn Trp Lys Val Asp Leu Val Asp Val Met Asp Glu Ile Ser	
775 780 785	
GGG AAC AGT CCC GCC GGG GTT TTT AAC AGT AAT GAG AAA TGG CAG AAA	8108
Gly Asn Ser Pro Ala Gly Val Phe Asn Ser Asn Glu Lys Trp Gln Lys	
790 795 800	
CAG CTG TAC TAC AGA GTA ACC GAT GGA AGA ACA TCG GTC CAG CTA ATG	8156
Gln Leu Tyr Tyr Arg Val Thr Asp Gly Arg Thr Ser Val Gln Leu Met	
805 810 815 820	
TGC CTG TCG TGC ACG AGC CAT TCT CCG GAA CCT TAC TGT CTT TTC GAC	8204
Cys Leu Ser Cys Thr Ser His Ser Pro Glu Pro Tyr Cys Leu Phe Asp	
825 830 835	
ACG TCT CTT ATA GCG AGG GAA AAA GAT ATC GCG CCA GAG TTA TAC TTT	8252
Thr Ser Leu Ile Ala Arg Glu Lys Asp Ile Ala Pro Glu Leu Tyr Phe	
840 845 850	
ACC TCT GAT CCG CAA ACG GCA TAC TGC ACA ATA ACT CTG CCG TCC GGC	8300
Thr Ser Asp Pro Gln Thr Ala Tyr Cys Thr Ile Thr Leu Pro Ser Gly	
855 860 865	
GTT GTT CCG AGA TTC GAA TGG AGC CTT AAT AAT GTT TCA CTG CCG GAA	8348
Val Val Pro Arg Phe Glu Trp Ser Leu Asn Asn Val Ser Leu Pro Glu	
870 875 880	
TAT TTG ACG GCC ACG ACC GTT GTT TCG CAT ACC GCT GGC CAA AGT ACA	8396
Tyr Leu Thr Ala Thr Thr Val Val Ser His Thr Ala Gly Gln Ser Thr	
885 890 895 900	
GTG TGG AAG AGC AGC GCG AGA GCA GGC GAG GCG TGG ATT TCT GGC CGG	8444
Val Trp Lys Ser Ser Ala Arg Ala Gly Glu Ala Trp Ile Ser Gly Arg	
905 910 915	
GGA GGC AAT ATA TAC GAA TGC ACC GTC CTC ATC TCA GAC GGC ACT CGC	8492
Gly Gly Asn Ile Tyr Glu Cys Thr Val Leu Ile Ser Asp Gly Thr Arg	
920 925 930	
GTT ACT ACG CGA AAG GAG AGG TGC TTA ACA AAC ACA TGG ATT GCG GTG	8540
Val Thr Thr Arg Lys Glu Arg Cys Leu Thr Asn Thr Trp Ile Ala Val	
935 940 945	
GAA AAC GGT GCT GCT CAG GCG CAG CTG TAT TCA CTC TTT TCT GGA CTT	8588
Glu Asn Gly Ala Ala Gln Ala Gln Leu Tyr Ser Leu Phe Ser Gly Leu	
950 955 960	
GTG TCA GGA TTA TGC GGG AGC ATA TCT GCT TTG TAC GCA ACG CTA TGG	8636
Val Ser Gly Leu Cys Gly Ser Ile Ser Ala Leu Tyr Ala Thr Leu Trp	
965 970 975 980	

099977 4425550

ACC GCC ATT TAT TTT TGAGGAATGC TTTTGGACT ATCGTACTGC TTTCTTCCTT 8691
 Thr Ala Ile Tyr Phe
 985

CGCTAGCCAG AGCACCGCCG CCGTCACGTA CGACTACATT TTAGGCCGTC GCGCGCTCGA 8751

CGCGCTAACC ATACCGGCGG TTGGCCCGTA TAACAGATAC CTCACTAGGG TATCAAGAGG 8811

CTGCGACGTT GTCGAGCTCA ACCCGATTTC TAACGTGGAC GACATGATAT CGGCGGCCAA 8871

AGAAAAAGAG AAGGGGGGCC CTTTCGAGGC CTCCGTCGTC TGGTTCTACG TGATTAAGGG 8931

CGACGACGGC GAGGACAAGT ACTGTCCAAT CTATAGAAAA GAGTACAGGG AATGTGGCGA 8991

CGTACAAC TG CTATCTGAAT GCGCCGTTCA ATCTGCACAG ATGTGGGCAG TGGACTATGT 9051

TCCTAGCACC CTTGTATCGC GAAATGGCGC GGGACTGACT ATATTCTCCC CCACTGCTGC 9111

GCTCTCTGGC CAATACTTGC TGACCCTGAA AATCGGGAGA TTTGCGCAAA CAGCTCTCGT 9171

AACTCTAGAA GTTAACGATC GCTGTTTAAA GATCGGGTCG CAGCTTAACT TTTTACCGTC 9231

GAAATGCTGG ACAACAGAAC AGTATCAGAC TGGATTTCAA GGCGAACACC TTTATCCGAT 9291

CGCAGACACC AATACACGAC ACGCGGACGA CGTATATCGG GGATACGAAG ATATTCTGCA 9351

GCGCTGGAAT AATTTGCTGA GGAAAAAGAA TCCTAGCGCG CCAGACCCTC GTCCAGATAG 9411

CGTCCCGCAA GAAATTCCTCG CTGTAACCAA GAAAGCGGAA GGGCGCACCC CGGACGCAGA 9471

AAGCAGCGAA AAGAAGGCC CTCCAGAAGA CTCGGAGGAC GACATGCAGG CAGAGGCTTC 9531

TGGAGAAAAT CCTGCCGCCC TCCCCGAAGA CGACGAAGTC CCCGAGGACA CCGAGCACGA 9591

TGATCCAAAC TCGGATCCTG ACTATTACAA TGACATGCCC GCCGTGATCC CGGTGGAGGA 9651

GACTACTAAA AGTTCTAATG CCGTCTCCAT GCCCATATTC GCGGCGTTTC TAGCCTGCGC 9711

GGTCGCGCTC GTGGGGCTAC TGGTTTGGAG CATCGTAAAA TGCGCGCGTA GCTAATCGAG 9771

CCTAGAATAG GTGGTTTCTT CCTACATGCC ACGCCTCACG CTCATAATAT AAATCACATG 9831

GAATAGCATA CCAATGCCTA TTCATTGGGA CGTTTCGAAAA GC 9873

ATG GCA TCG CTA CTT GGA ACT 9894
 Met Ala Ser Leu Leu Gly Thr
 1 5

CTG GCT CTC CTT GCC GCG ACG CTC GCA CCC TTC GGC GCG ATG GGA ATC 9942
 Leu Ala Leu Leu Ala Ala Thr Leu Ala Pro Phe Gly Ala Met Gly Ile
 10 15 20

GTG ATC ACT GGA AAT CAC GTC TCC GCC AGG ATT GAC GAC GAT CAC ATC 9990
 Val Ile Thr Gly Asn His Val Ser Ala Arg Ile Asp Asp Asp His Ile
 25 30 35

GTG ATC GTC GCG CCT CGC CCC GAA GCT ACA ATT CAA CTG CAG CTA TTT 10038
 Val Ile Val Ala Pro Arg Pro Glu Ala Thr Ile Gln Leu Gln Leu Phe
 40 45 50 55

TTC ATG CCT GGC CAG AGA CCC CAC AAA CCC TAC TCA GGA ACC GTC CGC 10086
 Phe Met Pro Gly Gln Arg Pro His Lys Pro Tyr Ser Gly Thr Val Arg
 60 65 70

GTC GCG TTT CGG TCT GAT ATA ACA AAC CAG TGC TAC CAG GAA CTT AGC 10134
 Val Ala Phe Arg Ser Asp Ile Thr Asn Gln Cys Tyr Gln Glu Leu Ser
 75 80 85

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GAG Glu	GAG Glu	CGC Arg 90	TTT Phe	GAA Glu	AAT Asn	TGC Cys	ACT Thr 95	CAT His	CGA Arg	TCG Ser	TCT Ser	TCT Ser 100	GTT Val	TTT Phe	GTC Val	10182
GGC Gly	TGT Cys 105	AAA Lys	GTG Val	ACC Thr	GAG Glu	TAC Tyr 110	ACG Thr	TTC Phe	TCC Ser	GCC Ala	TCG Ser 115	AAC Asn	AGA Arg	CTA Leu	ACC Thr	10230
GGA Gly 120	CCT Pro	CCA Pro	CAC His	CCG Pro	TTT Phe 125	AAG Lys	CTC Leu	ACT Thr	ATA Ile	CGA Arg 130	AAT Asn	CCT Pro	CGT Arg	CCG Pro	AAC Asn 135	10278
GAC Asp	AGC Ser	GGG Gly	ATG Met	TTC Phe 140	TAC Tyr	GTA Val	ATT Ile	GTT Val	CGG Arg 145	CTA Leu	GAC Asp	GAC Asp	ACC Thr	AAA Lys 150	GAA Glu	10326
CCC Pro	ATT Ile	GAC Asp	GTC Val 155	TTC Phe	GCG Ala	ATC Ile	CAA Gln	CTA Leu 160	TCG Ser	GTG Val	TAT Tyr	CAA Gln	TTC Phe 165	GCG Ala	AAC Asn	10374
ACC Thr	GCC Ala 170	GCG Ala	ACT Thr	CGC Arg	GGA Gly	CTC Leu	TAT Tyr 175	TCC Ser	AAG Lys	GCT Ala	TCG Ser	TGT Cys 180	CGC Arg	ACC Thr	TTC Phe	10422
GGA Gly 185	TTA Leu	CCT Pro	ACC Thr	GTC Val	CAA Gln	CTT Leu 190	GAG Glu	GCC Ala	TAT Tyr	CTC Leu	AGG Arg 195	ACC Thr	GAG Glu	GAA Glu	AGT Ser	10470
TGG Trp 200	CGC Arg	AAC Asn	TGG Trp	CAA Gln 205	GCG Ala	TAC Tyr	GTT Val	GCC Ala	ACG Thr	GAG Glu 210	GCC Ala	ACG Thr	ACG Thr	ACC Thr	AGC Ser 215	10518
GCC Ala	GAG Glu	GCG Ala	ACA Thr 220	ACC Thr	CCG Pro	ACG Thr	CCC Pro	GTC Val	ACT Thr 225	GCA Ala	ACC Thr	AGC Ser	GCC Ala	TCC Ser 230	GAA Glu	10566
CTT Leu	GAA Glu	GCG Ala	GAA Glu 235	CAC His	TTT Phe	ACC Thr	TTT Phe	CCC Pro 240	TGG Trp	CTA Leu	GAA Glu	AAT Asn	GGC Gly 245	GTG Val	GAT Asp	10614
CAT His	TAC Tyr 250	GAA Glu	CCG Pro	ACA Thr	CCC Pro	GCA Ala	AAC Asn 255	GAA Glu	AAT Asn	TCA Ser	AAC Asn	GTT Val 260	ACT Thr	GTC Val	CGT Arg	10662
CTC Leu 265	GGG Gly	ACA Thr	ATG Met	AGC Ser	CCT Pro	ACG Thr 270	CTA Leu	ATT Ile	GGG Gly	GTA Val	ACC Thr 275	GTG Val	GCT Ala	GCC Ala	GTC Val	10710
GTG Val 280	AGC Ser	GCA Ala	ACG Thr	ATC Ile	GGC Gly 285	CTC Leu	GTC Val	ATT Ile	GTA Val	ATT Ile 290	TCC Ser	ATC Ile	GTC Val	ACC Thr	AGA Arg 295	10758
AAC Asn	ATG Met	TGC Cys	ACC Thr 300	CCG Pro	CAC His	CGA Arg	AAA Lys	TTA Leu	GAC Asp 305	ACG Thr	GTC Val	TCG Ser	CAA Gln	GAC Asp 310	GAC Asp	10806
GAA Glu	GAA Glu	CGT Arg 315	TCC Ser	CAA Gln	ACT Thr	AGA Arg	AGG Arg	GAA Glu 320	TCG Ser	CGA Arg	AAA Lys	TTT Phe 325	GGA Gly	CCC Pro	ATG Met	10854
GTT Val	GCG Ala	TGC Cys 330	GAA Glu	ATA Ile	AAC Asn	AAG Lys	GGC Gly 335	GCT Ala	GAC Asp	CAG Gln	GAT Asp 340	AGT Ser	GAA Glu	CTT Leu	GTG Val	10902
GAA Glu 345	CTG Leu	GTT Val	GCG Ala	ATT Ile	GTT Val 350	AAC Asn	CCG Pro	TCT Ser	GCG Ala	CTA Leu 355	AGC Ser	TCG Ser	CCC Pro	GAC Asp	TCA Ser	10950

ATA AAA ATG TGATTAAGTC TGAATGTGGC TCTCCAATCA TTTCGATTCT	10999
Ile Lys Met	
360	
CTAATCTCCC AATCCTCTCA AAAGGGGCAG TATCGGACAC GGACTGGGAG GGGCGTACTA	11059
CACGATAGTT ATATGGTACA GCAGAGGCCT CTGAACACTT AGGAGGAGAA TTCAGCCGGG	11119
GAGAGCCCCT GTTGAGTAGG CTTGGGAGCA TATTGCAGG ATG AAC ATG TTA GTG	11173
Met Asn Met Leu Val	
1 5	
ATA GTT CTC GCC TCT TGT CTT GCG CGC CTA ACT TTT GCG ACG CGA CAC	11221
Ile Val Leu Ala Ser Cys Leu Ala Arg Leu Thr Phe Ala Thr Arg His	
10 15 20	
GTC CTC TTT TTG GAA GGC ACT CAG GCT GTC CTC GGG GAA GAT GAT CCC	11269
Val Leu Phe Leu Glu Gly Thr Gln Ala Val Leu Gly Glu Asp Asp Pro	
25 30 35	
AGA AAC GTT CCG GAA GGG ACT GTA ATC AAA TGG ACA AAA GTC CTG CGG	11317
Arg Asn Val Pro Glu Gly Thr Val Ile Lys Trp Thr Lys Val Leu Arg	
40 45 50	
AAC GCG TGC AAG ATG AAG GCG GCC GAT GTC TGC TCT TCG CCT AAC TAT	11365
Asn Ala Cys Lys Met Lys Ala Ala Asp Val Cys Ser Ser Pro Asn Tyr	
55 60 65	
TGC TTT CAT GAT TTA ATT TAC GAC GGA GGA AAG AAA GAC TGC CCG CCC	11413
Cys Phe His Asp Leu Ile Tyr Asp Gly Gly Lys Lys Asp Cys Pro Pro	
70 75 80 85	
GCG GGA CCC CTG TCT GCA AAC CTG GTA ATT TTA CTA AAG CGC GGC GAA	11461
Ala Gly Pro Leu Ser Ala Asn Leu Val Ile Leu Leu Lys Arg Gly Glu	
90 95 100	
AGC TTC GTC GTG CTG GGT TCT GGG CTA CAC AAC AGC AAT ATA ACT AAT	11509
Ser Phe Val Val Leu Gly Ser Gly Leu His Asn Ser Asn Ile Thr Asn	
105 110 115	
ATC ATG TGG ACA GAG TAC GGA GGC CTG CTC TTT GAT CCT GTA ACT CGT	11557
Ile Met Trp Thr Glu Tyr Gly Gly Leu Leu Phe Asp Pro Val Thr Arg	
120 125 130	
TCG GAC GAG GGA ATC TAT TTT CGA CGG ATC TCT CAG CCA GAT CTG GCC	11605
Ser Asp Glu Gly Ile Tyr Phe Arg Arg Ile Ser Gln Pro Asp Leu Ala	
135 140 145	
ATG GAA ACT ACA TCG TAC AAC GTC AGC GTT CTT TCG CAC GTA GAC GAG	11653
Met Glu Thr Thr Ser Tyr Asn Val Ser Val Leu Ser His Val Asp Glu	
150 155 160 165	
AAG GCT CCA GCA CCG CAC GAG GTG GAG ATA GAC ACC ATC AAG CCG TCA	11701
Lys Ala Pro Ala Pro His Glu Val Glu Ile Asp Thr Ile Lys Pro Ser	
170 175 180	
GAG GCC CAC GCG CAC GTG GAA TTA CAA ATG CTG CCG TTT CAT GAA CTC	11749
Glu Ala His Ala His Val Glu Leu Met Leu Pro Phe His Glu Leu	
185 190 195	
AAC GAC AAC AGC CCC ACC TAT GTG ACC CCT GTT CTT AGA GTC TTC CCA	11797
Asn Asp Asn Ser Pro Thr Tyr Val Thr Pro Val Leu Arg Val Phe Pro	
200 205 210	
CCG ACC GAG CAC GTA AAA TTT AAC GTT ACG TAT TCG TGG TAT GGG TTT	11845
Pro Thr Glu His Val Lys Phe Asn Val Thr Tyr Ser Trp Tyr Gly Phe	
215 220 225	

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GAT GTC AAA GAG GAG TGC GAA GAA GTG AAA CTG TTC GAG CCG TGC GTA Asp Val Lys Glu Glu Cys Glu Glu Val Lys Leu Phe Glu Pro Cys Val 230 235 240 245	11893
TAC CAT CCT ACA GAC GGC AAA TGT CAG TTT CCC GCA ACC AAC CAG AGA Tyr His Pro Thr Asp Gly Lys Cys Gln Phe Pro Ala Thr Asn Gln Arg 250 255 260	11941
TGC CTC ATA GGA TCT GTC TTG ATG GCG GAA TTC TTG GGC GCG GCC TCT Cys Leu Ile Gly Ser Val Leu Met Ala Glu Phe Leu Gly Ala Ala Ser 265 270 275	11989
TTG CTG GAT TGT TCC CGC GAT ACT CTA GAA GAC TGC CAC GAA AAT CGC Leu Leu Asp Cys Ser Arg Asp Thr Leu Glu Asp Cys His Glu Asn Arg 280 285 290	12037
GTG CCG AAC CTA CGG TTC GAT TCG CGA CTC TCC GAG TCA CGC GCA GGC Val Pro Asn Leu Arg Phe Asp Ser Arg Leu Ser Glu Ser Arg Ala Gly 295 300 305	12085
CTG GTG ATC AGT CCT CTT ATA GCC ATC CCC AAA GTT TTG ATT ATA GTC Leu Val Ile Ser Pro Leu Ile Ala Ile Pro Lys Val Leu Ile Ile Val 310 315 320 325	12133
GTT TCC GAC GGA GAC ATT TTG GGA TGG AGC TAC ACG GTG CTC GGG AAA Val Ser Asp Gly Asp Ile Leu Gly Trp Ser Tyr Thr Val Leu Gly Lys 330 335 340	12181
CGT AAC AGT CCG CGC GTA GTA GTC GAA ACG CAC ATG CCC TCG AAG GTC Arg Asn Ser Pro Arg Val Val Val Glu Thr His Met Pro Ser Lys Val 345 350 355	12229
CCG ATG AAC AAA GTA GTA ATT GGC AGT CCC GGA CCA ATG GAC GAA ACG Pro Met Asn Lys Val Val Ile Gly Ser Pro Gly Pro Met Asp Glu Thr 360 365 370	12277
GGT AAC TAT AAA ATG TAC TTC GTC GTC GCG GGG GTG GCC GCG ACG TGC Gly Asn Tyr Lys Met Tyr Phe Val Val Ala Gly Val Ala Ala Thr Cys 375 380 385	12325
GTA ATT CTT ACA TGC GCT CTG CTT GTG GGG AAA AAG AAG TGC CCC GCG Val Ile Leu Thr Cys Ala Leu Leu Val Gly Lys Lys Lys Cys Pro Ala 390 395 400 405	12373
CAC CAA ATG GGT ACT TTT TCC AAG ACC GAA CCA TTG TAC GCG CCG CTC His Gln Met Gly Thr Phe Ser Lys Thr Glu Pro Leu Tyr Ala Pro Leu 410 415 420	12421
CCC AAA AAC GAG TTT GAG GCC GGC GGG CTT ACG GAC GAT GAG GAA GTG Pro Lys Asn Glu Phe Glu Ala Gly Gly Leu Thr Asp Asp Glu Glu Val 425 430 435	12469
ATT TAT GAC GAA GTA TAC GAA CCC CTA TTT CGC GGC TAC TGT AAG CAG Ile Tyr Asp Glu Val Tyr Glu Pro Leu Phe Arg Gly Tyr Cys Lys Gln 440 445 450	12517
GAA TTC CGC GAA GAT GTG AAT ACC TTT TTC GGT GCG GTC GTG GAG GGA Glu Phe Arg Glu Asp Val Asn Thr Phe Phe Gly Ala Val Val Glu Gly 455 460 465	12565
GAA AGG GCC TTA AAC TTT AAA TCC GCC ATC GCA TCA ATG GCA GAT CGC Glu Arg Ala Leu Asn Phe Lys Ser Ala Ile Ala Ser Met Ala Asp Arg 470 475 480 485	12613
ATC CTG GCA AAT AAA AGC GGC AGA AGG AAT ATG GAT AGC TAT TAGTTGGTC Ile Leu Ala Asn Lys Ser Gly Arg Arg Asn Met Asp Ser Tyr 490 495 500	12664

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ATG CCT TTT AAG ACC AGA GGG GCC GAA GAC	12694
Met Pro Phe Lys Thr Arg Gly Ala Glu Asp	
1 5 10	
GCG GCC GCG GGC AAG AAC AGG TTT AAG AAA TCG AGA AAT CGG GAA ATC	12742
Ala Ala Ala Gly Lys Asn Arg Phe Lys Lys Ser Arg Asn Arg Glu Ile	
15 20 25	
TTA CCG ACC AGA CTG CGT GGC ACC GGT AAG AAA ACT GCC GGA TTG TCC	12790
Leu Pro Thr Arg Leu Arg Gly Thr Gly Lys Lys Thr Ala Gly Leu Ser	
30 35 40	
AAT TAT ACC CAG CCT ATT CCC TGG AAC CCT AAA TTC TGC AGC GCG CGC	12838
Asn Tyr Thr Gln Pro Ile Pro Trp Asn Pro Lys Phe Cys Ser Ala Arg	
45 50 55	
GGG GAA TCT GAC AAC CAC GCG TGT AAA GAC ACT TTT TAT CGC AGG ACG	12886
Gly Glu Ser Asp Asn His Ala Cys Lys Asp Thr Phe Tyr Arg Arg Thr	
60 65 70	
TGC TGC GCA TCG CGC TCT ACC GTT TCC AGT CAA CCC GAT TCC CCC CAC	12934
Cys Cys Ala Ser Arg Ser Thr Val Ser Ser Gln Pro Asp Ser Pro His	
75 80 85 90	
ACA CCC ATG CCT ACT GAG TAT GGG CGC GTG CCC TCC GCA AAG CGC AAA	12982
Thr Pro Met Pro Thr Glu Tyr Gly Arg Val Pro Ser Ala Lys Arg Lys	
95 100 105	
AAA CTA TCA TCT TCA GAC TSS GAG GGC GCG CAC CAA CCC CTA GTA TCC	13030
Lys Leu Ser Ser Ser Asp Xaa Glu Gly Ala His Gln Pro Leu Val Ser	
110 115 120	
TGT AAA CTT CCG GAT TCT CAA GCA GCA CCG GCG CGA ACC TAT AGT TCT	13078
Cys Lys Leu Pro Asp Ser Gln Ala Ala Pro Ala Arg Thr Tyr Ser Ser	
125 130 135	
GCG CAA AGA TAT ACT GTT GAC GAG GTT TCG TCG CCA ACT CCG CCA GGC	13126
Ala Gln Arg Tyr Thr Val Asp Glu Val Ser Ser Pro Thr Pro Pro Gly	
140 145 150	
GTC GAC GCT GTT GCG GAC TTA GAA ACG CGC GCG GAA CTT CCT GGC GCT	13174
Val Asp Ala Val Ala Asp Leu Glu Thr Arg Ala Glu Leu Pro Gly Ala	
155 160 165 170	
ACG ACG GAA CAA ACG GAA AGT AAA AAT AAG CTC CCC AAC CAA CAA TCG	13222
Thr Thr Glu Gln Thr Glu Ser Lys Asn Lys Leu Pro Asn Gln Gln Ser	
175 180 185	
CGC CTG AAG CCG AAA CCC ACA AAC GAG CAC GTC GGA GGG GAG CGG TGC	13270
Arg Leu Lys Pro Lys Pro Thr Asn Glu His Val Gly Gly Glu Arg Cys	
190 195 200	
CCC TCC GAA GGC ACG GTC GAG GCG CCA TCG CTC GGC ATC CTC TCG CGC	13318
Pro Ser Glu Gly Thr Val Glu Ala Pro Ser Leu Gly Ile Leu Ser Arg	
205 210 215	
GTC GGG GCA GCG ATA GCA AAC GAG CTG GCT CGT ATG CGG AGG GCG TGT	13366
Val Gly Ala Ala Ile Ala Asn Glu Leu Ala Arg Met Arg Arg Ala Cys	
220 225 230	
CTT CCG CTC GCC GCG TCG GCG GCC GCT GCC GGA ATA GTG GCC TGG GCC	13414
Leu Pro Leu Ala Ala Ser Ala Ala Ala Gly Ile Val Ala Trp Ala	
235 240 245 250	
GCG GCG AGG GCC TTG CAG AAA CAA GGG CGG TAG CAGTAATAATA ACCACACAA	13467
Ala Ala Arg Ala Leu Gln Lys Gln Gly Arg *	
255 260	

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ATATTG

13473

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 476 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Arg	Phe	Arg	Arg	Ile	Cys	Ser	Arg	Ser	Arg	Ala	Glu	Lys	Arg	Arg	1	5	10	15
Arg	Thr	Thr	Glu	Asn	Pro	Leu	Thr	Ser	Lys	Arg	Val	Cys	Val	Leu	Asp	20	25	30	
Ser	Phe	Ser	Arg	Thr	Met	Ser	Leu	Arg	Pro	Tyr	Ala	Glu	Ile	Leu	Pro	35	40	45	
Thr	Ala	Glu	Gly	Val	Glu	Arg	Leu	Ala	Glu	Leu	Val	Ser	Val	Thr	Met	50	55	60	
Thr	Glu	Arg	Ala	Glu	Pro	Val	Thr	Glu	Asn	Thr	Ala	Val	Asn	Ser	Ile	65	70	75	80
Pro	Pro	Ala	Asn	Glu	Asn	Gly	Gln	Asn	Phe	Ala	Tyr	Ala	Gly	Asp	Gly	85	90	95	
Pro	Ser	Thr	Thr	Glu	Lys	Val	Asp	Gly	Ser	His	Thr	Asp	Phe	Asp	Glu	100	105	110	
Ala	Ser	Ser	Asp	Tyr	Ala	Gly	Pro	Val	Pro	Leu	Ala	Gln	Thr	Arg	Leu	115	120	125	
Lys	His	Ser	Asp	Glu	Phe	Leu	Gln	His	Phe	Arg	Val	Leu	Asp	Asp	Leu	130	135	140	
Val	Glu	Gly	Ala	Tyr	Gly	Phe	Ile	Cys	Gly	Val	Arg	Arg	Tyr	Thr	Glu	145	150	155	160
Glu	Glu	Gln	Arg	Arg	Arg	Gly	Val	Asn	Ser	Thr	Asn	Gln	Gly	Lys	Ser	165	170	175	
Lys	Cys	Lys	Arg	Leu	Ile	Ala	Lys	Tyr	Val	Lys	Asn	Gly	Thr	Arg	Ala	180	185	190	
Ala	Ser	Gln	Leu	Glu	Asn	Glu	Ile	Leu	Val	Leu	Gly	Arg	Leu	Asn	His	195	200	205	
Glu	Asn	Val	Leu	Lys	Ile	Gln	Glu	Ile	Leu	Arg	Tyr	Pro	Asp	Asn	Thr	210	215	220	
Tyr	Met	Leu	Thr	Gln	Arg	Tyr	Gln	Phe	Asp	Leu	Tyr	Ser	Tyr	Met	Tyr	225	230	235	240
Asp	Glu	Ala	Phe	Asp	Trp	Lys	Asp	Ser	Pro	Met	Leu	Lys	Gln	Thr	Arg	245	250	255	
Arg	Ile	Met	Lys	Gln	Leu	Met	Ser	Ala	Val	Ser	Tyr	Ile	His	Ser	Lys	260	265	270	

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Lys Leu Ile His Arg Asp Ile Lys Leu Glu Asn Ile Phe Leu Asn Cys
275 280 285

Asp Gly Lys Thr Val Leu Gly Asp Phe Gly Thr Val Thr Pro Phe Glu
290 295 300

Asn Glu Arg Glu Pro Phe Glu Tyr Gly Trp Val Gly Thr Val Ala Thr
305 310 315 320

Asn Ser Pro Glu Ile Leu Ala Arg Asp Ser Tyr Cys Glu Ile Thr Asp
325 330 335

Ile Trp Ser Cys Gly Val Val Leu Leu Glu Met Val Ser His Glu Phe
340 345 350

Cys Pro Ile Gly Asp Gly Gly Gly Asn Pro His Gln Gln Leu Leu Lys
355 360 365

Val Ile Asp Ser Leu Ser Val Cys Asp Glu Glu Phe Pro Asp Pro Pro
370 375 380

Cys Asn Leu Tyr Asn Tyr Leu His Tyr Ala Ser Ile Asp Arg Ala Gly
385 390 395 400

His Thr Val Pro Ser Leu Ile Arg Asn Leu His Leu Pro Ala Asp Val
405 410 415

Glu Tyr Pro Leu Val Lys Met Leu Thr Phe Asp Trp Arg Leu Arg Pro
420 425 430

Ser Ala Ala Glu Val Leu Ala Met Pro Leu Phe Ser Ala Glu Glu Glu
435 440 445

Arg Thr Ile Thr Ile Ile His Gly Lys His Lys Pro Ile Arg Pro Glu
450 455 460

Ile Arg Ala Arg Val Pro Arg Ser Met Ser Glu Gly
465 470 475

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 510 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Thr Leu Pro His Arg Leu Thr Lys Arg Pro Phe Ala Arg Arg Phe
1 5 10 15

Cys Ser Val Phe Val Ile His Tyr Ser Glu Thr Lys Leu Asp Arg Tyr
20 25 30

Asn Lys Thr Met Leu Leu Tyr Arg Pro Asp Ser Thr Met Arg His Ser
35 40 45

Gly Gly Asp Ala Asn His Arg Gly Ile Arg Pro Arg Arg Lys Ser Ile
50 55 60

Gly Ala Phe Ser Ala Arg Glu Lys Thr Gly Lys Arg Asn Ala Leu Thr
65 70 75 80

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Glu	Ser	Ser	Ser	Ser	Ser	Asp	Met	Leu	Asp	Pro	Phe	Ser	Thr	Asp	Lys
				85					90					95	
Glu	Phe	Gly	Gly	Lys	Trp	Thr	Val	Asp	Gly	Pro	Ala	Asp	Ile	Thr	Ala
			100					105					110		
Glu	Val	Leu	Ser	Gln	Ala	Trp	Asp	Val	Leu	Gln	Leu	Val	Lys	His	Glu
		115					120					125			
Asp	Ala	Glu	Glu	Glu	Arg	Val	Thr	Tyr	Glu	Ser	Lys	Pro	Thr	Pro	Ile
	130					135					140				
Gln	Pro	Phe	Asn	Ala	Trp	Pro	Asp	Gly	Pro	Ser	Trp	Asn	Ala	Gln	Asp
145					150					155					160
Phe	Thr	Arg	Ala	Pro	Ile	Val	Tyr	Pro	Ser	Ala	Glu	Val	Leu	Asp	Ala
				165					170					175	
Glu	Ala	Leu	Lys	Val	Gly	Ala	Phe	Val	Ser	Arg	Val	Leu	Gln	Cys	Val
			180					185					190		
Pro	Phe	Thr	Arg	Ser	Lys	Lys	Ser	Val	Thr	Val	Arg	Asp	Ala	Gln	Ser
		195					200					205			
Phe	Leu	Gly	Asp	Ser	Phe	Trp	Arg	Ile	Met	Gln	Asn	Val	Tyr	Thr	Val
	210					215					220				
Cys	Leu	Arg	Gln	His	Ile	Thr	Arg	Leu	Arg	His	Pro	Ser	Ser	Lys	Ser
225					230					235					240
Ile	Val	Asn	Cys	Asn	Asp	Pro	Leu	Trp	Tyr	Ala	Tyr	Ala	Asn	Gln	Phe
				245					250					255	
His	Trp	Arg	Gly	Met	Arg	Val	Pro	Ser	Leu	Lys	Leu	Ala	Ser	Pro	Pro
			260					265					270		
Glu	Glu	Asn	Ile	Gln	His	Gly	Pro	Met	Ala	Ala	Val	Phe	Arg	Asn	Ala
		275					280					285			
Gly	Ala	Gly	Leu	Phe	Leu	Trp	Pro	Ala	Met	Arg	Ala	Ala	Phe	Glu	Glu
	290					295					300				
Arg	Asp	Lys	Arg	Leu	Leu	Arg	Ala	Cys	Leu	Ser	Ser	Leu	Asp	Ile	Met
305					310					315					320
Asp	Ala	Ala	Val	Leu	Ala	Ser	Phe	Pro	Phe	Tyr	Trp	Arg	Gly	Val	Gln
				325					330					335	
Asp	Thr	Ser	Arg	Phe	Glu	Pro	Ala	Leu	Gly	Cys	Leu	Ser	Glu	Tyr	Phe
			340					345					350		
Ala	Leu	Val	Val	Leu	Leu	Ala	Glu	Thr	Val	Leu	Ala	Thr	Met	Phe	Asp
		355					360					365			
His	Ala	Leu	Val	Phe	Met	Arg	Ala	Leu	Ala	Asp	Gly	Asn	Phe	Asp	Asp
	370					375					380				
Tyr	Asp	Glu	Thr	Arg	Tyr	Ile	Asp	Pro	Val	Lys	Asn	Glu	Tyr	Leu	Asn
385					390					395					400
Gly	Ala	Glu	Gly	Thr	Leu	Leu	Arg	Gly	Ile	Val	Ala	Ser	Asn	Thr	Ala
				405					410					415	
Leu	Ala	Val	Val	Cys	Ala	Asn	Thr	Tyr	Ser	Thr	Ile	Arg	Lys	Leu	Pro
			420					425					430		

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Ser Val Ala Thr Ser Ala Cys Asn Val Ala Tyr Arg Thr Glu Thr Leu
435 440 445
Lys Ala Arg Arg Pro Gly Met Ser Asp Ile Tyr Arg Ile Leu Gln Lys
450 455 460
Glu Phe Phe Phe Tyr Ile Ala Trp Leu Gln Arg Val Ala Thr His Ala
465 470 475 480
Asn Phe Cys Leu Asn Ile Leu Lys Arg Ser Val Asp Thr Gly Pro Arg
485 490 495
His Phe Cys Ser Gly Pro Ala Arg Arg Ser Gly Cys Ser Ser
500 505 510

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 110 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Leu Cys Pro Leu Leu Val Pro Ile Gln Tyr Glu Asp Phe Ser Lys
1 5 10 15
Ala Met Gly Ser Glu Leu Lys Arg Glu Lys Leu Glu Thr Phe Val Lys
20 25 30
Ala Ile Ser Ser Asp Arg Asp Pro Arg Gly Ser Leu Arg Phe Leu Ile
35 40 45
Ser Asp His Ala Arg Glu Ile Ile Ala Asp Gly Val Arg Phe Lys Pro
50 55 60
Val Ile Asp Glu Pro Val Arg Ala Ser Val Ala Leu Ser Thr Ala Ala
65 70 75 80
Ala Gly Lys Val Lys Ala Arg Arg Leu Thr Ser Val Arg Ala Pro Val
85 90 95
Pro Pro Ala Gly Ala Val Ser Ala Arg Arg Lys Ser Glu Ile
100 105 110

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 292 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Ser Gly Phe Ser Asn Ile Gly Ser Ile Ala Thr Val Ser Leu Val
1 5 10 15
Cys Ser Leu Leu Cys Ala Ser Val Leu Gly Ala Pro Val Leu Asp Gly
20 25 30

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Leu Glu Ser Ser Pro Phe Pro Phe Gly Gly Lys Ile Ile Ala Gln Ala
35 40 45
Cys Asn Arg Thr Thr Ile Glu Val Thr Val Pro Trp Ser Asp Tyr Ser
50 55 60
Gly Arg Thr Glu Gly Val Ser Val Glu Val Lys Trp Phe Tyr Gly Asn
65 70 75 80
Ser Asn Pro Glu Ser Phe Val Phe Gly Val Asp Ser Glu Thr Gly Ser
85 90 95
Gly His Glu Asp Leu Ser Thr Cys Trp Ala Leu Ile His Asn Leu Asn
100 105 110
Ala Ser Val Cys Arg Ala Ser Asp Ala Gly Ile Pro Asp Phe Asp Lys
115 120 125
Gln Cys Glu Lys Val Gln Arg Arg Leu Arg Ser Gly Val Glu Leu Gly
130 135 140
Ser Tyr Val Ser Gly Asn Gly Ser Leu Val Leu Tyr Pro Gly Met Tyr
145 150 155 160
Asp Ala Gly Ile Tyr Ala Tyr Gln Leu Ser Val Gly Gly Lys Gly Tyr
165 170 175
Thr Gly Ser Val Tyr Leu Asp Val Gly Pro Asn Pro Gly Cys His Asp
180 185 190
Gln Tyr Gly Tyr Thr Tyr Tyr Ser Leu Ala Asp Glu Ala Ser Asp Leu
195 200 205
Ser Ser Tyr Asp Val Ala Ser Pro Glu Leu Asp Gly Pro Met Glu Glu
210 215 220
Asp Tyr Ser Asn Cys Leu Asp Met Pro Pro Leu Arg Pro Trp Thr Thr
225 230 235 240
Val Cys Ser His Asp Val Glu Glu Gln Glu Asn Ala Thr Asp Glu Leu
245 250 255
Tyr Leu Trp Asp Glu Glu Cys Ala Gly Pro Leu Asp Glu Tyr Val Asp
260 265 270
Glu Arg Ser Glu Thr Met Pro Arg Met Val Val Phe Ser Pro Pro Ser
275 280 285
Thr Leu Gln Gln
290

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 985 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Gly Thr Met Leu Val Leu Arg Leu Phe Leu Leu Ala Val Ala Asp
1 5 10 15

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Ala	Ala	Leu	Pro	Thr	Gly	Arg	Phe	Cys	Arg	Val	Trp	Lys	Val	Pro	Pro
		20						25					30		
Gly	Gly	Thr	Ile	Gln	Glu	Asn	Leu	Ala	Val	Leu	Ala	Glu	Ser	Pro	Val
		35					40					45			
Thr	Gly	His	Ala	Thr	Tyr	Pro	Pro	Pro	Glu	Gly	Ala	Val	Ser	Phe	Gln
	50					55					60				
Ile	Phe	Ala	Asp	Thr	Pro	Thr	Leu	Arg	Ile	Arg	Tyr	Gly	Pro	Thr	Glu
	65				70					75					80
Asp	Glu	Leu	Ala	Leu	Glu	Arg	Gly	Thr	Ser	Ala	Ser	Asp	Ala	Asp	Asn
				85					90					95	
Val	Thr	Phe	Ser	Leu	Ser	Tyr	Arg	Pro	Arg	Pro	Glu	Ile	His	Gly	Ala
			100					105					110		
Tyr	Phe	Thr	Ile	Gly	Val	Phe	Ala	Thr	Gly	Gln	Ser	Thr	Glu	Ser	Ser
		115					120					125			
Tyr	Ser	Val	Ile	Ser	Arg	Val	Leu	Val	Asn	Ala	Ser	Leu	Glu	Arg	Ser
	130					135					140				
Val	Arg	Leu	Glu	Thr	Pro	Cys	Asp	Glu	Asn	Phe	Leu	Gln	Asn	Glu	Pro
	145				150					155					160
Thr	Trp	Gly	Ser	Lys	Arg	Trp	Leu	Gly	Pro	Pro	Ser	Pro	Tyr	Val	Arg
				165					170					175	
Asp	Asn	Asp	Val	Ala	Val	Leu	Thr	Lys	Ala	Gln	Tyr	Ile	Gly	Glu	Cys
			180					185					190		
Tyr	Ser	Asn	Ser	Ala	Ala	Gln	Thr	Gly	Leu	Thr	Ser	Leu	Asn	Met	Thr
		195				200						205			
Phe	Phe	Tyr	Ser	Pro	Lys	Arg	Ile	Val	Asn	Val	Thr	Trp	Thr	Thr	Gly
	210					215					220				
Gly	Pro	Ser	Pro	Ser	Arg	Ile	Thr	Val	Tyr	Ser	Ser	Arg	Glu	Asn	Gly
	225				230					235				240	
Gln	Pro	Val	Leu	Arg	Asn	Val	Ser	Asp	Gly	Phe	Leu	Val	Lys	Tyr	Thr
				245					250					255	
Pro	Asp	Ile	Asp	Gly	Arg	Ala	Met	Ile	Asn	Val	Ile	Ala	Asn	Tyr	Ser
			260					265					270		
Pro	Ala	Asp	Ser	Gly	Ser	Val	Leu	Ala	Phe	Thr	Ala	Phe	Arg	Glu	Gly
		275					280					285			
Lys	Leu	Pro	Ser	Ala	Ile	Gln	Leu	His	Arg	Ile	Asp	Met	Ser	Gly	Thr
	290					295					300				
Glu	Pro	Pro	Gly	Thr	Glu	Thr	Thr	Phe	Asp	Cys	Gln	Lys	Met	Ile	Glu
	305				310					315					320
Thr	Pro	Tyr	Arg	Ala	Leu	Gly	Ser	Asn	Val	Pro	Arg	Asp	Asp	Ser	Ile
				325					330					335	
Arg	Pro	Gly	Ala	Thr	Leu	Pro	Pro	Phe	Asp	Thr	Ala	Ala	Pro	Asp	Phe
			340					345					350		
Asp	Thr	Gly	Thr	Ser	Pro	Thr	Pro	Thr	Thr	Val	Pro	Glu	Pro	Ala	Ile
		355					360					365			

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Thr Thr Leu Ile Pro Arg Ser Thr Ser Asp Met Gly Phe Phe Ser Thr
370 375 380

Ala Arg Ala Thr Gly Ser Glu Thr Leu Ser Val Pro Val Gln Glu Thr
385 390 400

Asp Arg Thr Leu Ser Thr Thr Pro Leu Thr Leu Pro Leu Thr Pro Gly
405 410 415

Glu Ser Glu Asn Thr Leu Phe Pro Thr Thr Ala Pro Gly Ile Ser Thr
420 425 430

Glu Thr Pro Ser Ala Ala His Glu Thr Thr Gln Thr Gln Ser Ala Glu
435 440 445

Thr Val Val Phe Thr Gln Ser Pro Ser Thr Glu Ser Glu Thr Ala Arg
450 455 460

Ser Gln Ser Gln Glu Pro Trp Tyr Phe Thr Gln Thr Pro Ser Thr Glu
465 470 475 480

Gln Ala Ala Leu Thr Gln Thr Gln Ile Ala Glu Thr Glu Ala Leu Phe
485 490 495

Thr Gln Thr Pro Ser Ala Glu Gln Met Thr Phe Thr Gln Thr Pro Gly
500 505 510

Ala Glu Thr Glu Ala Pro Ala Gln Thr Pro Ser Thr Ile Pro Glu Ile
515 520 525

Phe Thr Gln Ser Arg Ser Thr Pro Pro Glu Thr Ala Arg Ala Pro Ser
530 535 540

Ala Ala Pro Glu Val Phe Thr Gln Ser Ser Ser Thr Val Thr Glu Val
545 550 555 560

Phe Thr Gln Thr Pro Ser Thr Val Pro Lys Thr Thr Leu Ser Ser Ser
565 570 575

Thr Glu Pro Ala Ile Phe Thr Arg Thr Gln Ser Ala Gly Thr Glu Ala
580 585 590

Phe Thr Gln Thr Ser Ser Ala Glu Pro Asp Thr Met Arg Thr Gln Ser
595 600 605

Thr Glu Thr His Phe Phe Thr Gln Ala Pro Ser Thr Val Pro Lys Ala
610 615 620

Thr Gln Thr Pro Ser Thr Glu Pro Glu Val Leu Thr Gln Ser Pro Ser
625 630 635 640

Thr Glu Pro Val Pro Phe Thr Arg Thr Leu Gly Ala Glu Pro Glu Ile
645 650 655

Thr Gln Thr Pro Ser Ala Ala Pro Glu Val Tyr Thr Arg Ser Ser Ser
660 665 670

Thr Met Pro Glu Thr Ala Gln Ser Thr Pro Leu Ala Ser Gln Asn Pro
675 680 685

Thr Ser Ser Gly Thr Gly Thr His Asn Thr Glu Pro Arg Thr Tyr Pro
690 695 700

Val Gln Thr Thr Pro His Thr Gln Lys Leu Tyr Thr Glu Asn Lys Thr
705 710 715 720

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Leu Ser Phe Pro Thr Val Val Ser Glu Phe His Glu Met Ser Thr Ala
725 730 735

Glu Ser Gln Thr Pro Leu Leu Asp Val Lys Ile Val Glu Val Lys Phe
740 745 750

Ser Asn Asp Gly Glu Val Thr Ala Thr Cys Val Ser Thr Val Lys Ser
755 760 765

Pro Tyr Arg Val Glu Thr Asn Trp Lys Val Asp Leu Val Asp Val Met
770 775 780

Asp Glu Ile Ser Gly Asn Ser Pro Ala Gly Val Phe Asn Ser Asn Glu
785 790 795 800

Lys Trp Gln Lys Gln Leu Tyr Tyr Arg Val Thr Asp Gly Arg Thr Ser
805 810 815

Val Gln Leu Met Cys Leu Ser Cys Thr Ser His Ser Pro Glu Pro Tyr
820 825 830

Cys Leu Phe Asp Thr Ser Leu Ile Ala Arg Glu Lys Asp Ile Ala Pro
835 840 845

Glu Leu Tyr Phe Thr Ser Asp Pro Gln Thr Ala Tyr Cys Thr Ile Thr
850 855 860

Leu Pro Ser Gly Val Val Pro Arg Phe Glu Trp Ser Leu Asn Asn Val
865 870 875 880

Ser Leu Pro Glu Tyr Leu Thr Ala Thr Thr Val Val Ser His Thr Ala
885 890 895

Gly Gln Ser Thr Val Trp Lys Ser Ser Ala Arg Ala Gly Glu Ala Trp
900 905 910

Ile Ser Gly Arg Gly Gly Asn Ile Tyr Glu Cys Thr Val Leu Ile Ser
915 920 925

Asp Gly Thr Arg Val Thr Thr Arg Lys Glu Arg Cys Leu Thr Asn Thr
930 935 940

Trp Ile Ala Val Glu Asn Gly Ala Ala Gln Ala Gln Leu Tyr Ser Leu
945 950 955 960

Phe Ser Gly Leu Val Ser Gly Leu Cys Gly Ser Ile Ser Ala Leu Tyr
965 970 975

Ala Thr Leu Trp Thr Ala Ile Tyr Phe
980 985

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 362 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ala Ser Leu Leu Gly Thr Leu Ala Leu Leu Ala Ala Thr Leu Ala
1 5 10 15

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Pro Phe Gly Ala Met Gly Ile Val Ile Thr Gly Asn His Val Ser Ala
20 25 30

Arg Ile Asp Asp Asp His Ile Val Ile Val Ala Pro Arg Pro Glu Ala
35 40 45

Thr Ile Gln Leu Gln Leu Phe Phe Met Pro Gly Gln Arg Pro His Lys
50 55 60

Pro Tyr Ser Gly Thr Val Arg Val Ala Phe Arg Ser Asp Ile Thr Asn
65 70 75 80

Gln Cys Tyr Gln Glu Leu Ser Glu Glu Arg Phe Glu Asn Cys Thr His
85 90 95

Arg Ser Ser Ser Val Phe Val Gly Cys Lys Val Thr Glu Tyr Thr Phe
100 105 110

Ser Ala Ser Asn Arg Leu Thr Gly Pro Pro His Pro Phe Lys Leu Thr
115 120 125

Ile Arg Asn Pro Arg Pro Asn Asp Ser Gly Met Phe Tyr Val Ile Val
130 135 140

Arg Leu Asp Asp Thr Lys Glu Pro Ile Asp Val Phe Ala Ile Gln Leu
145 150 155 160

Ser Val Tyr Gln Phe Ala Asn Thr Ala Ala Thr Arg Gly Leu Tyr Ser
165 170 175

Lys Ala Ser Cys Arg Thr Phe Gly Leu Pro Thr Val Gln Leu Glu Ala
180 185 190

Tyr Leu Arg Thr Glu Glu Ser Trp Arg Asn Trp Gln Ala Tyr Val Ala
195 200 205

Thr Glu Ala Thr Thr Thr Ser Ala Glu Ala Thr Thr Pro Thr Pro Val
210 215 220

Thr Ala Thr Ser Ala Ser Glu Leu Glu Ala Glu His Phe Thr Phe Pro
225 230 235 240

Trp Leu Glu Asn Gly Val Asp His Tyr Glu Pro Thr Pro Ala Asn Glu
245 250 255

Asn Ser Asn Val Thr Val Arg Leu Gly Thr Met Ser Pro Thr Leu Ile
260 265 270

Gly Val Thr Val Ala Ala Val Val Ser Ala Thr Ile Gly Leu Val Ile
275 280 285

Val Ile Ser Ile Val Thr Arg Asn Met Cys Thr Pro His Arg Lys Leu
290 295 300

Asp Thr Val Ser Gln Asp Asp Glu Glu Arg Ser Gln Thr Arg Arg Glu
305 310 315 320

Ser Arg Lys Phe Gly Pro Met Val Ala Cys Glu Ile Asn Lys Gly Ala
325 330 335

Asp Gln Asp Ser Glu Leu Val Glu Leu Val Ala Ile Val Asn Pro Ser
340 345 350

Ala Leu Ser Ser Pro Asp Ser Ile Lys Met
355 360

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(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 499 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Asn	Met	Leu	Val	Ile	Val	Leu	Ala	Ser	Cys	Leu	Ala	Arg	Leu	Thr	1	5	10	15
Phe	Ala	Thr	Arg	His	Val	Leu	Phe	Leu	Glu	Gly	Thr	Gln	Ala	Val	Leu	20	25	30	
Gly	Glu	Asp	Asp	Pro	Arg	Asn	Val	Pro	Glu	Gly	Thr	Val	Ile	Lys	Trp	35	40	45	
Thr	Lys	Val	Leu	Arg	Asn	Ala	Cys	Lys	Met	Lys	Ala	Ala	Asp	Val	Cys	50	55	60	
Ser	Ser	Pro	Asn	Tyr	Cys	Phe	His	Asp	Leu	Ile	Tyr	Asp	Gly	Gly	Lys	65	70	75	
Lys	Asp	Cys	Pro	Pro	Ala	Gly	Pro	Leu	Ser	Ala	Asn	Leu	Val	Ile	Leu	85	90	95	
Leu	Lys	Arg	Gly	Glu	Ser	Phe	Val	Val	Leu	Gly	Ser	Gly	Leu	His	Asn	100	105	110	
Ser	Asn	Ile	Thr	Asn	Ile	Met	Trp	Thr	Glu	Tyr	Gly	Gly	Leu	Leu	Phe	115	120	125	
Asp	Pro	Val	Thr	Arg	Ser	Asp	Glu	Gly	Ile	Tyr	Phe	Arg	Arg	Ile	Ser	130	135	140	
Gln	Pro	Asp	Leu	Ala	Met	Glu	Thr	Thr	Ser	Tyr	Asn	Val	Ser	Val	Leu	145	150	155	
Ser	His	Val	Asp	Glu	Lys	Ala	Pro	Ala	Pro	His	Glu	Val	Glu	Ile	Asp	165	170	175	
Thr	Ile	Lys	Pro	Ser	Glu	Ala	His	Ala	His	Val	Glu	Leu	Gln	Met	Leu	180	185	190	
Pro	Phe	His	Glu	Leu	Asn	Asp	Asn	Ser	Pro	Thr	Tyr	Val	Thr	Pro	Val	195	200	205	
Leu	Arg	Val	Phe	Pro	Pro	Thr	Glu	His	Val	Lys	Phe	Asn	Val	Thr	Tyr	210	215	220	
Ser	Trp	Tyr	Gly	Phe	Asp	Val	Lys	Glu	Glu	Cys	Glu	Glu	Val	Lys	Leu	225	230	235	
Phe	Glu	Pro	Cys	Val	Tyr	His	Pro	Thr	Asp	Gly	Lys	Cys	Gln	Phe	Pro	245	250	255	
Ala	Thr	Asn	Gln	Arg	Cys	Leu	Ile	Gly	Ser	Val	Leu	Met	Ala	Glu	Phe	260	265	270	
Leu	Gly	Ala	Ala	Ser	Leu	Leu	Asp	Cys	Ser	Arg	Asp	Thr	Leu	Glu	Asp	275	280	285	
Cys	His	Glu	Asn	Arg	Val	Pro	Asn	Leu	Arg	Phe	Asp	Ser	Arg	Leu	Ser	290	295	300	

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Glu Ser Arg Ala Gly Leu Val Ile Ser Pro Leu Ile Ala Ile Pro Lys
305 310 315 320

Val Leu Ile Ile Val Val Ser Asp Gly Asp Ile Leu Gly Trp Ser Tyr
325 330 335

Thr Val Leu Gly Lys Arg Asn Ser Pro Arg Val Val Val Glu Thr His
340 345 350

Met Pro Ser Lys Val Pro Met Asn Lys Val Val Ile Gly Ser Pro Gly
355 360 365

Pro Met Asp Glu Thr Gly Asn Tyr Lys Met Tyr Phe Val Val Ala Gly
370 375 380

Val Ala Ala Thr Cys Val Ile Leu Thr Cys Ala Leu Leu Val Gly Lys
385 390 395 400

Lys Lys Cys Pro Ala His Gln Met Gly Thr Phe Ser Lys Thr Glu Pro
405 410 415

Leu Tyr Ala Pro Leu Pro Lys Asn Glu Phe Glu Ala Gly Gly Leu Thr
420 425 430

Asp Asp Glu Glu Val Ile Tyr Asp Glu Val Tyr Glu Pro Leu Phe Arg
435 440 445

Gly Tyr Cys Lys Gln Glu Phe Arg Glu Asp Val Asn Thr Phe Phe Gly
450 455 460

Ala Val Val Glu Gly Glu Arg Ala Leu Asn Phe Lys Ser Ala Ile Ala
465 470 475 480

Ser Met Ala Asp Arg Ile Leu Ala Asn Lys Ser Gly Arg Arg Asn Met
485 490 495

Asp Ser Tyr

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 260 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Pro Phe Lys Thr Arg Gly Ala Glu Asp Ala Ala Ala Gly Lys Asn
1 5 10 15

Arg Phe Lys Lys Ser Arg Asn Arg Glu Ile Leu Pro Thr Arg Leu Arg
20 25 30

Gly Thr Gly Lys Lys Thr Ala Gly Leu Ser Asn Tyr Thr Gln Pro Ile
35 40 45

Pro Trp Asn Pro Lys Phe Cys Ser Ala Arg Gly Glu Ser Asp Asn His
50 55 60

Ala Cys Lys Asp Thr Phe Tyr Arg Arg Thr Cys Cys Ala Ser Arg Ser
65 70 75 80

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Thr Val Ser Ser Gln Pro Asp Ser Pro His Thr Pro Met Pro Thr Glu
85 90 95
Tyr Gly Arg Val Pro Ser Ala Lys Arg Lys Lys Leu Ser Ser Ser Asp
100 105 110
Xaa Glu Gly Ala His Gln Pro Leu Val Ser Cys Lys Leu Pro Asp Ser
115 120 125
Gln Ala Ala Pro Ala Arg Thr Tyr Ser Ser Ala Gln Arg Tyr Thr Val
130 135 140
Asp Glu Val Ser Ser Pro Thr Pro Pro Gly Val Asp Ala Val Ala Asp
145 150 155 160
Leu Glu Thr Arg Ala Glu Leu Pro Gly Ala Thr Thr Glu Gln Thr Glu
165 170 175
Ser Lys Asn Lys Leu Pro Asn Gln Gln Ser Arg Leu Lys Pro Lys Pro
180 185 190
Thr Asn Glu His Val Gly Gly Glu Arg Cys Pro Ser Glu Gly Thr Val
195 200 205
Glu Ala Pro Ser Leu Gly Ile Leu Ser Arg Val Gly Ala Ala Ile Ala
210 215 220
Asn Glu Leu Ala Arg Met Arg Arg Ala Cys Leu Pro Leu Ala Ala Ser
225 230 235 240
Ala Ala Ala Ala Gly Ile Val Ala Trp Ala Ala Ala Arg Ala Leu Gln
245 250 255
Lys Gln Gly Arg
260

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1305 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..1305

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATG CAC CGT CCT CAT CTC AGA CGG CAC TCG CGT TAC TAC GCG AAA GGA	48
Met His Arg Pro His Leu Arg Arg His Ser Arg Tyr Tyr Ala Lys Gly	
1 5 10 15	
GAG GTG CTT AAC AAA CAC ATG GAT TGC GGT GGA AAA CGG TGC TGC TCA	96
Glu Val Leu Asn Lys His Met Asp Cys Gly Gly Lys Arg Cys Cys Ser	
20 25 30	

GGC GCA GCT GTA TTC ACT CTT TTC TGG ACT TGT GTC AGG ATT ATG CGG	144
Gly Ala Ala Val Phe Thr Leu Phe Trp Thr Cys Val Arg Ile Met Arg	
35 40 45	
GAG CAT ATC TGC TTT GTA CGC AAC GCT ATG GAC CGC CAT TTA TTT TTG	192
Glu His Ile Cys Phe Val Arg Asn Ala Met Asp Arg His Leu Phe Leu	
50 55 60	
AGG AAT GCT TTT TGG ACT ATC GTA CTG CTT TCT TCC TTC GCT AGC CAG	240
Arg Asn Ala Phe Trp Thr Ile Val Leu Leu Ser Ser Phe Ala Ser Gln	
65 70 75 80	
AGC ACC GCC GCC GTC ACG TAC GAC TAC ATT TTA GGC CGT CGC GCG CTC	288
Ser Thr Ala Ala Val Thr Tyr Asp Tyr Ile Leu Gly Arg Arg Ala Leu	
85 90 95	
GAC GCG CTA ACC ATA CCG GCG GTT GGC CCG TAT AAC AGA TAC CTC ACT	336
Asp Ala Leu Thr Ile Pro Ala Val Gly Pro Tyr Asn Arg Tyr Leu Thr	
100 105 110	
AGG GTA TCA AGA GGC TGC GAC GTT GTC GAG CTC AAC CCG ATT TCT AAC	384
Arg Val Ser Arg Gly Cys Asp Val Val Glu Leu Asn Pro Ile Ser Asn	
115 120 125	
GTG GAC GAC ATG ATA TCG GCG GCC AAA GAA AAA GAG AAG GGG GGC CCT	432
Val Asp Asp Met Ile Ser Ala Ala Lys Glu Lys Glu Lys Gly Gly Pro	
130 135 140	
TTC GAG GCC TCC GTC GTC TGG TTC TAC GTG ATT AAG GGC GAC GAC GGC	480
Phe Glu Ala Ser Val Val Trp Phe Tyr Val Ile Lys Gly Asp Asp Gly	
145 150 155 160	
GAG GAC AAG TAC TGT CCA ATC TAT AGA AAA GAG TAC AGG GAA TGT GGC	528
Glu Asp Lys Tyr Cys Pro Ile Tyr Arg Lys Glu Tyr Arg Glu Cys Gly	
165 170 175	
GAC GTA CAA CTG CTA TCT GAA TGC GCC GTT CAA TCT GCA CAG ATG TGG	576
Asp Val Gln Leu Leu Ser Glu Cys Ala Val Gln Ser Ala Gln Met Trp	
180 185 190	
GCA GTG GAC TAT GTT CCT AGC ACC CTT GTA TCG CGA AAT GGC GCG GGA	624
Ala Val Asp Tyr Val Pro Ser Thr Leu Val Ser Arg Asn Gly Ala Gly	
195 200 205	
CTG ACT ATA TTC TCC CCC ACT GCT GCG CTC TCT GGC CAA TAC TTG CTG	672
Leu Thr Ile Phe Ser Pro Thr Ala Ala Leu Ser Gly Gln Tyr Leu Leu	
210 215 220	
ACC CTG AAA ATC GGG AGA TTT GCG CAA ACA GCT CTC GTA ACT CTA GAA	720
Thr Leu Lys Ile Gly Arg Phe Ala Gln Thr Ala Leu Val Thr Leu Glu	
225 230 235 240	
GTT AAC GAT CGC TGT TTA AAG ATC GGG TCG CAG CTT AAC TTT TTA CCG	768
Val Asn Asp Arg Cys Leu Lys Ile Gly Ser Gln Leu Asn Phe Leu Pro	
245 250 255	
TCG AAA TGC TGG ACA ACA GAA CAG TAT CAG ACT GGA TTT CAA GGC GAA	816
Ser Lys Cys Trp Thr Thr Glu Gln Tyr Gln Thr Gly Phe Gln Gly Glu	
260 265 270	
CAC CTT TAT CCG ATC GCA GAC ACC AAT ACA CGA CAC GCG GAC GAC GTA	864
His Leu Tyr Pro Ile Ala Asp Thr Asn Thr Arg His Ala Asp Asp Val	
275 280 285	
TAT CGG GGA TAC GAA GAT ATT CTG CAG CGC TGG AAT AAT TTG CTG AGG	912
Tyr Arg Gly Tyr Glu Asp Ile Leu Gln Arg Trp Asn Asn Leu Leu Arg	
290 295 300	

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AAA AAG AAT CCT AGC GCG CCA GAC CCT CGT CCA GAT AGC GTC CCG CAA	960
Lys Lys Asn Pro Ser Ala Pro Asp Pro Arg Pro Asp Ser Val Pro Gln	
305 310 315 320	
GAA ATT CCC GCT GTA ACC AAG AAA GCG GAA GGG CGC ACC CCG GAC GCA	1008
Glu Ile Pro Ala Val Thr Lys Lys Ala Glu Gly Arg Thr Pro Asp Ala	
325 330 335	
GAA AGC AGC GAA AAG AAG GCC CCT CCA GAA GAC TCG GAG GAC GAC ATG	1056
Glu Ser Ser Glu Lys Lys Ala Pro Pro Glu Asp Ser Glu Asp Asp Met	
340 345 350	
CAG GCA GAG GCT TCT GGA GAA AAT CCT GCC GCC CTC CCC GAA GAC GAC	1104
Gln Ala Glu Ala Ser Gly Glu Asn Pro Ala Ala Leu Pro Glu Asp Asp	
355 360 365	
GAA GTC CCC GAG GAC ACC GAG CAC GAT GAT CCA AAC TCG GAT CCT GAC	1152
Glu Val Pro Glu Asp Thr Glu His Asp Asp Pro Asn Ser Asp Pro Asp	
370 375 380	
TAT TAC AAT GAC ATG CCC GCC GTG ATC CCG GTG GAG GAG ACT ACT AAA	1200
Tyr Tyr Asn Asp Met Pro Ala Val Ile Pro Val Glu Glu Thr Thr Lys	
385 390 395 400	
AGT TCT AAT GCC GTC TCC ATG CCC ATA TTC GCG GCG TTC GTA GCC TGC	1248
Ser Ser Asn Ala Val Ser Met Pro Ile Phe Ala Ala Phe Val Ala Cys	
405 410 415	
GCG GTC GCG CTC GTG GGG CTA CTG GTT TGG AGC ATC GTA AAA TGC GCG	1296
Ala Val Ala Leu Val Gly Leu Leu Val Trp Ser Ile Val Lys Cys Ala	
420 425 430	
CGT AGC TAA	1305
Arg Ser	
435	

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 434 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met His Arg Pro His Leu Arg Arg His Ser Arg Tyr Tyr Ala Lys Gly	
1 5 10 15	
Glu Val Leu Asn Lys His Met Asp Cys Gly Gly Lys Arg Cys Cys Ser	
20 25 30	
Gly Ala Ala Val Phe Thr Leu Phe Trp Thr Cys Val Arg Ile Met Arg	
35 40 45	
Glu His Ile Cys Phe Val Arg Asn Ala Met Asp Arg His Leu Phe Leu	
50 55 60	
Arg Asn Ala Phe Trp Thr Ile Val Leu Leu Ser Ser Phe Ala Ser Gln	
65 70 75 80	
Ser Thr Ala Ala Val Thr Tyr Asp Tyr Ile Leu Gly Arg Arg Ala Leu	
85 90 95	

[illegible]

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 690 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATG GCG CCT GTA AAA GTG ACT ATA GTT TCT GCG GTC GAT TCG CAC TAC	48
Met Ala Pro Val Lys Val Thr Ile Val Ser Ala Val Asp Ser His Tyr	
1 5 10 15	
AAA CTA CCT AAT TCT AGA TTT GAG CTC TCG GAT TCT GGA TGG AAA GAA	96
Lys Leu Pro Asn Ser Arg Phe Glu Leu Ser Asp Ser Gly Trp Lys Glu	
20 25 30	
TTG GTT CAC GCA GTG AAA ACT ATG GCG AGT TAC GAT CGT CCG AGT ACA	144
Leu Val His Ala Val Lys Thr Met Ala Ser Tyr Asp Arg Pro Ser Thr	
35 40 45	
TTA TCG GTA ATC GTG CGC CCG GCA TCT CTG TAC GAA GTT TCC GGG GAG	192
Leu Ser Val Ile Val Arg Pro Ala Ser Leu Tyr Glu Val Ser Gly Glu	
50 55 60	
CTG TTT TCC CTT CCC AGG ATG TGC AGA CCC GTG ATT CGG TTC GGT GAG	240
Leu Phe Ser Leu Pro Arg Met Cys Arg Pro Val Ile Arg Phe Gly Glu	
65 70 75 80	
GGG GGC GAC CCG CCT GGA GTA AGT CCC GAG TGG AGC GGC TTG GAC GCA	288
Gly Gly Asp Pro Gly Val Ser Pro Glu Trp Ser Gly Leu Asp Ala	
85 90 95	
GGG TTT TAC CAT TTG TCA TCT GGC GCG TAT GCC GCA AAA GAG TTC CAT	336
Gly Phe Tyr His Leu Ser Ser Gly Ala Tyr Ala Ala Lys Glu Phe His	
100 105 110	
TTG TGG GTG CTG GGT ACC GCT GAC ATA TGC ATG GCA GCT TTA AAC CTC	384
Leu Trp Val Leu Gly Thr Ala Asp Ile Cys Met Ala Ala Leu Asn Leu	
115 120 125	
CCT GCG CCA AAA ACT TTC CTA ATT ACC GAA ACC GGA GGT AAA AAT TTT	432
Pro Ala Pro Lys Thr Phe Leu Ile Thr Glu Thr Gly Gly Lys Asn Phe	
130 135 140	
GAG AGA GGA GTG GAA ATA TTT TTG GTA AAC GGA GAC AAG ACA ACG CTG	480
Glu Arg Gly Val Glu Ile Phe Leu Val Asn Gly Asp Lys Thr Thr Leu	
145 150 155 160	
TCT CTG AGT CAC CCA TCA GTC TGG ACA ACT CTT GCC CCT TCG AGC CTG	528
Ser Leu Ser His Pro Ser Val Trp Thr Thr Leu Ala Pro Ser Ser Leu	
165 170 175	

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AGA	ACG	CCC	TGG	CCG	TAC	AGC	ACG	GTA	AAG	TTT	TTA	AAA	GTA	AAA	CCT	576
Arg	Thr	Pro	Trp	Pro	Tyr	Ser	Thr	Val	Lys	Phe	Leu	Lys	Val	Lys	Pro	
			180					185					190			
AAC	TCG	GCC	GCA	TAC	TGT	GTT	TCC	GAC	TCG	GAT	GAT	GGC	GAA	CGG	CAG	624
Asn	Ser	Ala	Ala	Tyr	Cys	Val	Ser	Asp	Ser	Asp	Asp	Gly	Glu	Arg	Gln	
		195					200					205				
CCA	AAA	TTT	TTT	CTC	GGG	AGT	CTA	TTT	AAG	TCG	AAG	AAA	CCC	CGC	TCC	672
Pro	Lys	Phe	Phe	Leu	Gly	Ser	Leu	Phe	Lys	Ser	Lys	Lys	Pro	Arg	Ser	
	210					215					220					
CCG	CGG	CGC	CGA	CGT	TA	G										690
Pro	Arg	Arg	Arg	Arg												
225																

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 229 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met	Ala	Pro	Val	Lys	Val	Thr	Ile	Val	Ser	Ala	Val	Asp	Ser	His	Tyr	
1				5					10					15		
Lys	Leu	Pro	Asn	Ser	Arg	Phe	Glu	Leu	Ser	Asp	Ser	Gly	Trp	Lys	Glu	
			20					25					30			
Leu	Val	His	Ala	Val	Lys	Thr	Met	Ala	Ser	Tyr	Asp	Arg	Pro	Ser	Thr	
		35					40					45				
Leu	Ser	Val	Ile	Val	Arg	Pro	Ala	Ser	Leu	Tyr	Glu	Val	Ser	Gly	Glu	
	50					55					60					
Leu	Phe	Ser	Leu	Pro	Arg	Met	Cys	Arg	Pro	Val	Ile	Arg	Phe	Gly	Glu	
	65				70					75					80	
Gly	Gly	Asp	Pro	Pro	Gly	Val	Ser	Pro	Glu	Trp	Ser	Gly	Leu	Asp	Ala	
				85					90					95		
Gly	Phe	Tyr	His	Leu	Ser	Ser	Gly	Ala	Tyr	Ala	Ala	Lys	Glu	Phe	His	
			100					105					110			
Leu	Trp	Val	Leu	Gly	Thr	Ala	Asp	Ile	Cys	Met	Ala	Ala	Leu	Asn	Leu	
		115					120					125				
Pro	Ala	Pro	Lys	Thr	Phe	Leu	Ile	Thr	Glu	Thr	Gly	Gly	Lys	Asn	Phe	
	130					135					140					
Glu	Arg	Gly	Val	Glu	Ile	Phe	Leu	Val	Asn	Gly	Asp	Lys	Thr	Thr	Leu	
	145				150					155					160	
Ser	Leu	Ser	His	Pro	Ser	Val	Trp	Thr	Thr	Leu	Ala	Pro	Ser	Ser	Leu	
				165					170					175		
Arg	Thr	Pro	Trp	Pro	Tyr	Ser	Thr	Val	Lys	Phe	Leu	Lys	Val	Lys	Pro	
			180					185					190			
Asn	Ser	Ala	Ala	Tyr	Cys	Val	Ser	Asp	Ser	Asp	Asp	Gly	Glu	Arg	Gln	
		195					200					205				

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Pro Lys Phe Phe Leu Gly Ser Leu Phe Lys Ser Lys Lys Pro Arg Ser
210 215 220

Pro Arg Arg Arg Arg
225

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 381 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..380

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATG CGT AGC TCA GTT ACG TCA TTG TGG AGC CCT TCA GAT CAC GCC TCT	48
Met Arg Ser Ser Val Thr Ser Leu Trp Ser Pro Ser Asp His Ala Ser	
1 5 10 15	
TCG CCC GCA AAT GCC AAG CAT TTT TAT CAT ATT TCC GAT TTC CGG CGC	96
Ser Pro Ala Asn Ala Lys His Phe Tyr His Ile Ser Asp Phe Arg Arg	
20 25 30	
GCG GAA ACG GCG CCT GCG GGC GGT ACG GGC GCG CGA ACT GAG GTT AAG	144
Ala Glu Thr Ala Pro Ala Gly Gly Thr Gly Ala Arg Thr Glu Val Lys	
35 40 45	
CGT CGC GCT TTC ACT TTC CCA GCG GCA GCG GTA CTC AGC GCA ACT GAA	192
Arg Arg Ala Phe Thr Phe Pro Ala Ala Ala Val Leu Ser Ala Thr Glu	
50 55 60	
GCC CGA ACC GGC TCG TCT ATC ACC GGC TTA AAC CGT ACT CCG TCT GCA	240
Ala Arg Thr Gly Ser Ser Ile Thr Gly Leu Asn Arg Thr Pro Ser Ala	
65 70 75 80	
ATA ATT TCC CTT GCA TGG TCC GAA ATG AGA AAT CTT AAG GAC CCC CTC	288
Ile Ile Ser Leu Ala Trp Ser Glu Met Arg Asn Leu Lys Asp Pro Leu	
85 90 95	
GGG TCC CTG TCG CTG GAA ATA GCT TTA ACG AAT GTC TCT AAC TTT TCC	336
Gly Ser Leu Ser Leu Glu Ile Ala Leu Thr Asn Val Ser Asn Phe Ser	
100 105 110	
CTC TTG AGC TCA GAC CCC ATG GCC TTC GAA AAG TCT TCA TAT TG	380
Leu Leu Ser Ser Asp Pro Met Ala Phe Glu Lys Ser Ser Tyr	
115 120 125	
A	381

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 126 amino acids

T09077 "425660"

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

```
Met Arg Ser Ser Val Thr Ser Leu Trp Ser Pro Ser Asp His Ala Ser
 1           5           10           15
Ser Pro Ala Asn Ala Lys His Phe Tyr His Ile Ser Asp Phe Arg Arg
          20           25           30
Ala Glu Thr Ala Pro Ala Gly Gly Thr Gly Ala Arg Thr Glu Val Lys
          35           40           45
Arg Arg Ala Phe Thr Phe Pro Ala Ala Ala Val Leu Ser Ala Thr Glu
          50           55           60
Ala Arg Thr Gly Ser Ser Ile Thr Gly Leu Asn Arg Thr Pro Ser Ala
          65           70           75           80
Ile Ile Ser Leu Ala Trp Ser Glu Met Arg Asn Leu Lys Asp Pro Leu
          85           90           95
Gly Ser Leu Ser Leu Glu Ile Ala Leu Thr Asn Val Ser Asn Phe Ser
          100          105          110
Leu Leu Ser Ser Asp Pro Met Ala Phe Glu Lys Ser Ser Tyr
          115          120          125
```

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 879 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..878

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```
ATG TGG TGT CGT TTG CAC TGG ATA AGT CCT CGG TTC AGT ATT ATG CGT      48
Met Trp Cys Arg Leu His Trp Ile Ser Pro Arg Phe Ser Ile Met Arg
 1           5           10           15

CCC GGT TCC CGA ACT GGT AGG GTT TTG CGA GGC CAG GGG TGT GCT CTG      96
Pro Gly Ser Arg Thr Gly Arg Val Leu Arg Gly Gln Gly Cys Ala Leu
          20           25           30

TGC AGT TTC TGG CAT CGT ACT CGA ACT CCG AGT ATA AAC CTC CGG TGC      144
Cys Ser Phe Trp His Arg Thr Arg Thr Pro Ser Ile Asn Leu Arg Cys
          35           40           45
```

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CGC GCT CGG GGT CTG AGT AAT TTC CGG CTC TGC GCC CAG AGT CCG GGT Arg Ala Arg Gly Leu Ser Asn Phe Arg Leu Cys Ala Gln Ser Pro Gly 50 55 60	192
GAA AGG CAC AGG TTC GGT ACT CGG ACT CTG AGT CAA CAC CTC CGG CTC Glu Arg His Arg Phe Gly Thr Arg Thr Leu Ser Gln His Leu Arg Leu 65 70 75 80	240
TGT ACT CGG AGT CTG AGT AGC TTT CGG TAC CGT ACT CGG GGC CTG AGT Cys Thr Arg Ser Leu Ser Ser Phe Arg Tyr Arg Thr Arg Gly Leu Ser 85 90 95	288
GAA AAA GTG TGT TTC AGT ACT CTG AGT TCG CAT AGT GTC CGG CTC GGC Glu Lys Val Cys Phe Ser Thr Leu Ser Ser His Ser Val Arg Leu Gly 100 105 110	336
ACT CGA AGT CTG AGT AAA GGC CTC AGT TCC CGC GCT CTG AGT CCG AGT Thr Arg Ser Leu Ser Lys Gly Leu Ser Ser Arg Ala Leu Ser Pro Ser 115 120 125	384
AAA AAT CGC CGG TTC AGT ACT CGA ACT CAG AGT AGT TTT CGG TAC CGT Lys Asn Arg Arg Phe Ser Thr Arg Thr Gln Ser Ser Phe Arg Tyr Arg 130 135 140	432
GCT CGG GGT CTG AGT AAA CAC CTC CGT TAC CGT ACT CGA ACT CTG TGT Ala Arg Gly Leu Ser Lys His Leu Arg Tyr Arg Thr Arg Thr Leu Cys 145 150 155 160	480
AAA AAC CTC CGG CGC CGC GCT CGG AGC GCG AGC GGT TTC GGG GGG CGT Lys Asn Leu Arg Arg Arg Ala Arg Ser Ala Ser Gly Phe Gly Gly Arg 165 170 175	528
GCT ACG AGA CTG AGT AAA TAT CTC GGG TAT CGT GCT CGG GGT CTG GGC Ala Thr Arg Leu Ser Lys Tyr Leu Gly Tyr Arg Ala Arg Gly Leu Gly 180 185 190	576
AGG TGC CTC GGT TTC TGC ACC CGG AGT CTG AGT AAA AGT CAT CTG TTC Arg Cys Leu Gly Phe Cys Thr Arg Ser Leu Ser Lys Ser His Leu Phe 195 200 205	624
AGC ACT CGG AGT CTG AGT AAA CAA CGC CTC CGT TTC TGC GAT CTG CGT Ser Thr Arg Ser Leu Ser Lys Gln Arg Leu Arg Phe Cys Asp Leu Arg 210 215 220	672
CTG AGT AAG AGC CGC CTG TTC AGT ACT CGG AGT CTG AGT AAA ATA CCA Leu Ser Lys Ser Arg Leu Phe Ser Thr Arg Ser Leu Ser Lys Ile Pro 225 230 235 240	720
CGG TTC CTG ACT CTG GGA CCG CGC GGT TTC CGA CTC GGT ACT CGG ACT Arg Phe Leu Thr Leu Gly Pro Arg Gly Phe Arg Leu Gly Thr Arg Thr 245 250 255	768
CTG AGT AAA GAC CAC CGT TTC TGC ACT CTG GGT CTG TGT AGT TTC ATG Leu Ser Lys Asp His Arg Phe Cys Thr Leu Gly Leu Cys Ser Phe Met 260 265 270	816
TGC CGC GCT CGG GGT CTC GGT AGA AAT CCC CGG CGC GGT CGT AGG AAA Cys Arg Ala Arg Gly Leu Gly Arg Asn Pro Arg Arg Gly Arg Arg Lys 275 280 285	864
CAG TGT ATT TTC TG A Gln Ile Phe 290	879

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 292 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met	Trp	Cys	Arg	Leu	His	Trp	Ile	Ser	Pro	Arg	Phe	Ser	Ile	Met	Arg
1				5					10					15	
Pro	Gly	Ser	Arg	Thr	Gly	Arg	Val	Leu	Arg	Gly	Gln	Gly	Cys	Ala	Leu
			20					25					30		
Cys	Ser	Phe	Trp	His	Arg	Thr	Arg	Thr	Pro	Ser	Ile	Asn	Leu	Arg	Cys
		35				40						45			
Arg	Ala	Arg	Gly	Leu	Ser	Asn	Phe	Arg	Leu	Cys	Ala	Gln	Ser	Pro	Gly
	50					55					60				
Glu	Arg	His	Arg	Phe	Gly	Thr	Arg	Thr	Leu	Ser	Gln	His	Leu	Arg	Leu
	65				70					75					80
Cys	Thr	Arg	Ser	Leu	Ser	Ser	Phe	Arg	Tyr	Arg	Thr	Arg	Gly	Leu	Ser
				85					90					95	
Glu	Lys	Val	Cys	Phe	Ser	Thr	Leu	Ser	Ser	His	Ser	Val	Arg	Leu	Gly
			100					105					110		
Thr	Arg	Ser	Leu	Ser	Lys	Gly	Leu	Ser	Ser	Arg	Ala	Leu	Ser	Pro	Ser
		115					120					125			
Lys	Asn	Arg	Arg	Phe	Ser	Thr	Arg	Thr	Gln	Ser	Ser	Phe	Arg	Tyr	Arg
	130					135					140				
Ala	Arg	Gly	Leu	Ser	Lys	His	Leu	Arg	Tyr	Arg	Thr	Arg	Thr	Leu	Cys
	145				150				155						160
Lys	Asn	Leu	Arg	Arg	Arg	Ala	Arg	Ser	Ala	Ser	Gly	Phe	Gly	Gly	Arg
				165					170					175	
Ala	Thr	Arg	Leu	Ser	Lys	Tyr	Leu	Gly	Tyr	Arg	Ala	Arg	Gly	Leu	Gly
			180					185					190		
Arg	Cys	Leu	Gly	Phe	Cys	Thr	Arg	Ser	Leu	Ser	Lys	Ser	His	Leu	Phe
		195					200					205			
Ser	Thr	Arg	Ser	Leu	Ser	Lys	Gln	Arg	Leu	Arg	Phe	Cys	Asp	Leu	Arg
	210					215					220				
Leu	Ser	Lys	Ser	Arg	Leu	Phe	Ser	Thr	Arg	Ser	Leu	Ser	Lys	Ile	Pro
	225				230					235					240
Arg	Phe	Leu	Thr	Leu	Gly	Pro	Arg	Gly	Phe	Arg	Leu	Gly	Thr	Arg	Thr
				245				250						255	
Leu	Ser	Lys	Asp	His	Arg	Phe	Cys	Thr	Leu	Gly	Leu	Cys	Ser	Phe	Met
			260					265					270		
Cys	Arg	Ala	Arg	Gly	Leu	Gly	Arg	Asn	Pro	Arg	Arg	Gly	Arg	Arg	Lys
		275					280					285			
Gln	Cys	Ile	Phe												
	290														

(2) INFORMATION FOR SEQ ID NO:18:

0099377 22E5660

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 534 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..533
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ATG CTC CCA AGC CTA CTC AAC AGG GGC TCT CCC CGG CTG AAT TCT CCT	48
Met Leu Pro Ser Leu Leu Asn Arg Gly Ser Pro Arg Leu Asn Ser Pro	
1 5 10 15	
CCT AAG TGT TCA GAG GCC TCT GCT GTA CCA TAT AAC TAT CGT GTA GTA	96
Pro Lys Cys Ser Glu Ala Ser Ala Val Pro Tyr Asn Tyr Arg Val Val	
20 25 30	
CGC CCC TCC CAG TCC GTG TCC GAT ACT GCC CCT TTT GAG AGG ATT GGG	144
Arg Pro Ser Gln Ser Val Ser Asp Thr Ala Pro Phe Glu Arg Ile Gly	
35 40 45	
AGA TTA GAG AAT CGA AAT GAT TGG AGA GCC ACA TTC AGA CTT AAT CAC	192
Arg Leu Glu Asn Arg Asn Asp Trp Arg Ala Thr Phe Arg Leu Asn His	
50 55 60	
ATT TTT ATT GAG TCG GGC GAG CTT AGC GCA GAC GGG TTA ACA ATC GCA	240
Ile Phe Ile Glu Ser Gly Glu Leu Ser Ala Asp Gly Leu Thr Ile Ala	
65 70 75 80	
ACC AGT TCC ACA AGT TCA CTA TCC TGG TCA GCG CCC TTG TTT ATT TCG	288
Thr Ser Ser Thr Ser Ser Leu Ser Trp Ser Ala Pro Leu Phe Ile Ser	
85 90 95	
CAC GCA ACC ATG GGT CCA AAT TTT CGC GAT TCC CTT CTA GTT TGG GAA	336
His Ala Thr Met Gly Pro Asn Phe Arg Asp Ser Leu Leu Val Trp Glu	
100 105 110	
CGT TCT TCG TCG TCT TGC GAG ACC GTG TCT AAT TTT CGG TGC GGG GTG	384
Arg Ser Ser Ser Ser Cys Glu Thr Val Ser Asn Phe Arg Cys Gly Val	
115 120 125	
CAC ATG TTT CTG GTG ACG ATG GAA ATT ACA ATG ACG AGG CCG ATC GTT	432
His Met Phe Leu Val Thr Met Glu Ile Thr Met Thr Arg Pro Ile Val	
130 135 140	
GCG CTC ACG ACG GCA GCC ACG GTT ACC CCA ATT AGC GTA GGG CTC ATT	480
Ala Leu Thr Thr Ala Thr Val Thr Pro Ile Ser Val Gly Leu Ile	
145 150 155 160	
GTC CCG AGA CGG ACA GTA ACG TTT GAA TTT TCG TTT GCG GGT GTC GGT	528
Val Pro Arg Arg Thr Val Thr Phe Glu Phe Ser Phe Ala Gly Val Gly	
165 170 175	
TCG TA A	534
Ser	

099377 110601

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 177 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Leu Pro Ser Leu Leu Asn Arg Gly Ser Pro Arg Leu Asn Ser Pro
 1 5 10 15
 Pro Lys Cys Ser Glu Ala Ser Ala Val Pro Tyr Asn Tyr Arg Val Val
 20 25 30
 Arg Pro Ser Gln Ser Val Ser Asp Thr Ala Pro Phe Glu Arg Ile Gly
 35 40 45
 Arg Leu Glu Asn Arg Asn Asp Trp Arg Ala Thr Phe Arg Leu Asn His
 50 55 60
 Ile Phe Ile Glu Ser Gly Glu Leu Ser Ala Asp Gly Leu Thr Ile Ala
 65 70 75 80
 Thr Ser Ser Thr Ser Ser Leu Ser Trp Ser Ala Pro Leu Phe Ile Ser
 85 90 95
 His Ala Thr Met Gly Pro Asn Phe Arg Asp Ser Leu Leu Val Trp Glu
 100 105 110
 Arg Ser Ser Ser Ser Cys Glu Thr Val Ser Asn Phe Arg Cys Gly Val
 115 120 125
 His Met Phe Leu Val Thr Met Glu Ile Thr Met Thr Arg Pro Ile Val
 130 135 140
 Ala Leu Thr Thr Ala Ala Thr Val Thr Pro Ile Ser Val Gly Leu Ile
 145 150 155 160
 Val Pro Arg Arg Thr Val Thr Phe Glu Phe Ser Phe Ala Gly Val Gly
 165 170 175
 Ser

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 48 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GAATTCGAGC TCGGTACCCG GATAATACGT ACATGTTAAC GCAGAGGT

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GCTGACCGCT AGTCGACCTG CAGTGAATAA TAAAAT

36

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TGTCCGTCGA GATCCTCTAG AGTCGACGAA AGGTCAGAGA CGATGCCC

48

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CGGATCAGAA ACTCTTTCGG TACCCGGGAT CCTCTAGA

38

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

0099377 110601

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GAATACAAGC TTAGATGCAT ATTTACTCGA GCC

33

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GGTTTGGCGG AGCGGATATG ATCTCGACCT GCAGTGAATA ATAAAATGTG T

51

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TGTCCGTCGA GATCCTCTAG AGTCGAGATC AGCAAAATGT TCACGGGG

48

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

009977 226550

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

AAGCTTGGCG TAATCATG

18

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GGAATTCGAG CTCGGTACCT CGTGGCGAGC GCAGGCGGC

39

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 51 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GGCCGAGTTA GGTTTTACTT TTCTAGAGGA TCCCCTCGAC GTCTGGGGCG C

51

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TTGCTGCGTT CCCGGGGATC CTCTAGAATT AGGTAGTTTG TAGTGCGA

48

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:

0099377 110601
T0907T " 226660

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TCAAGATCCA GGAAATCCTT CGGTACCGAG CTCGAATTCG TA

42

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GAATTCGAGC TCGGTACCGA AAGCTACTCA GAC

33

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CGCAAACAGC TCTCGTAACT CTAGAAGTTA ACGATCGCTG TT

42

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 57 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

09937 1001
T000T 226660

(iv) ANTI-SENSE: NO

GAATAGCATA CCAATGCCTA TTCATTGGGA CTCGACTCTA GAGGATCCCC GGGAACG

(2) INFORMATION FOR SEQ ID NO:35:

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

TCGAGGGGAT CCTCTAGAGT CGAGGGACCC ATGGTTGCGT GC

(2) INFORMATION FOR SEQ ID NO:36:

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

TTTACTAAAG CGCGGCGAAA GCTTCGTCGT GCTGGGTTCT GG

(2) INFORMATION FOR SEQ ID NO:37:

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

AAGCTTGGCG TAATCATGGT C

21

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GGAATTCGAG CTCGGTACCC GGATAATACG TACATGTTAA CGCAGAGG

48

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

ATCTATTGGA GCGTTTAGCG CGCGTCGACG AAAGGTCAGA GACGA

45

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CTGCTTCATT TCTGATCCCC GGGAACG

27

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:

09937 10601
T0907T 226660

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(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
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ACCACCCCCG CGCCCCAGAC GTCGAGGGGA TCAATTATTG CGTATTGAAT A

51

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

ATCAGAAACT CTTTCGGTAC CGAGCTCGAA TTC

33

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GAATTCGAGC TCGGTACCCG GATAATACGT ACATGTTAAC GCAGAGGT

48

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

GCTGACCGCT AGTCGACTCT AGAGGATCCC CTC

33

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CGTTCCCGGG GATCCTCTAG AGTCGACGGC AGAGTCGCAG AC

42

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TGATCCAAAC TCGGATCCTC TAGAGTCGAC

30

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 48 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

AAGCTTGGGC TGCAGGTCGA CTCTAGAGGA TCCCCTCGAC GTCTGGGG

48

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CACACCTTTG CGCATCTCCA CAGCTCAACA ATGAATTCCA TGTTACGTCC TGTAGAAACC

60

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CAGGGAGGCA AACAAATGAAT CAACAACCTCT CCCGGGAGAT GGGGGAGGCT AACTGAAACA

60

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

TGCTGCGTTC CCGGGGATCC TCTAGAGTCG ACCTGCAGCC CAAGC

45

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:

009937 226660
T0907 110601

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

TCTAGAGTCG ACCTGCAGTG AATAATAAAA TGTGTGTTTG TCCGAAAT

48

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

CTCCATAGAA GACACCGGGA CCATGGATCC CGTCGTTTCA CAACG

45

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TCGGCGGAAA TCCAGCTGAG CGCCGGTCGC TACCATTACC AGTTGGTCTG GTGTCAAAAA
GATCTAGAAT AAGCTAGAGG ATCGATCCCC TATGGCGATC ATCAG

60

105

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CGCCTCGAGG ACCCATGGTT GCGTGCG

27

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CTCGTCCGAA CGAGTTACAG

20

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18912 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 697..1533
- (D) OTHER INFORMATION:

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: complement (1900..2784)
- (D) OTHER INFORMATION:

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: complement (2916..3605)
- (D) OTHER INFORMATION:

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3694..5124
- (D) OTHER INFORMATION:

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 5210..7081
- (D) OTHER INFORMATION:

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 7245..8123
- (D) OTHER INFORMATION:

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 8333..11290
- (D) OTHER INFORMATION:

(ix) FEATURE:

- (A) NAME/KEY: CDS

0099377 "110601

- (B) LOCATION: 11098..12402
(D) OTHER INFORMATION:
- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 12510..13598
(D) OTHER INFORMATION:
- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 13792..15291
(D) OTHER INFORMATION:
- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 15298..16080
(D) OTHER INFORMATION:
- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 16129..17013
(D) OTHER INFORMATION:
- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: complement (17380..18216)
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GGATCCCGAA GAGCTCTCCC AGAAGTTTTT CTTTTCGGAC GTATCGGAGG ACGAAGAACC	60
GGCACGCGGG AGGAGCTGGA GCGACCCGGA GTCGGAGGAA GAGCAGCCTG GGTGCCGGGG	120
AGTGGACTTG GCGGAGGAGG ACACGGGACA CAGCTCCACC GAGTCAGAGC CCACGCAATC	180
TGACTTAGAC TTTATTGACG ACAGCTCTCC GGCGCCGCCG CCATTTGCTA TCCCCCGCGT	240
CCGTGCGTTA TTGCGGTGCG CGGCACCCGC AAAGACCCAC GGAAGGCTTC GGCCGCCAGG	300
GCGGGTAGGC GCACTCTTAA AAGACGGAGG TTGTCATTTT CTTCTTCCTC TGACGAGGAA	360
TCCGAGGAGA GAAGTAAAAA AGAAGAAGCG GCCTCGACCC CTGCACGGCG ACGCAAGGCC	420
GAGGCCTCGA CGAGCAGATA GAGGAGACGC GGGGCAGAAC CTCCCCCTCC CTCCCACCCC	480
CCTACTCTGG ACATTTATTG CCCGCTCGAT CCATTCTCAT CCAGAACTTC TTTCCCCTC	540
AGCCTTCACG CAGAAGCGGA CGCGCGCCCC TTTGCGACCG CCGGACATCC CGCCGCCCCC	600
CCCCCTTCAC GCCCGGCGCA ATCCGTAGCC GTCCAACCTCG GCCCAGCACA ACCGCAGTAG	660
ACCGCCCGGA CCGCTCTCCT CTAGACACAT CCCTAA ATG GAA AAC ATG CTC GAC	714
Met Glu Asn Met Leu Asp	
1 5	
GGG TGC TAC CCG CTG GCG CTG ATG GAC AGC GAT CAC ATT ACT GCG CAC	762
Gly Cys Tyr Pro Leu Ala Leu Met Asp Ser Asp His Ile Thr Ala His	
10 15 20	
GCG GTA CCT CGT GGC GAG CGC AGG CGG CAA GGT GCC GCT GTC GCC TCG	810
Ala Val Pro Arg Gly Glu Arg Arg Gln Gly Ala Val Ala Ser	
25 30 35	
TCG GAG TCG GCC GAC TCG GTA GAC CCG TGC ATT CGG ATC GCC TCG CGG	858
Ser Glu Ser Ala Asp Ser Val Arg Pro Cys Ile Arg Ile Ala Ser Arg	
40 45 50	
CTC TGG CGC GAG TTA GTC GAG ATA TCG TCC GAA CTC AAG GAC GGT TAC	906
Leu Trp Arg Glu Leu Val Glu Ile Ser Ser Glu Leu Lys Asp Gly Tyr	
55 60 65 70	

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GGA GAG TTC ACG TCA GCG AGA GAC CGC CGC AAC GCG CTG ATT GCT GCC	954
Gly Glu Phe Thr Ser Ala Arg Asp Arg Arg Asn Ala Leu Ile Ala Ala	
75 80 85	
AAC GAA CGG CTA CGT TCG GCT TTT CTG GGG GCC AGC CGG GCG ACG CGC	1002
Asn Glu Arg Leu Arg Ser Ala Phe Leu Gly Ala Ser Arg Ala Thr Arg	
90 95 100	
GGC CTA GGT TTG AGG CCG CGG TGG GCG TCG ACG GAG AGC GTC GCC AAC	1050
Gly Leu Gly Leu Arg Pro Arg Trp Ala Ser Thr Glu Ser Val Ala Asn	
105 110 115	
TCC CCC ACT GAC CCG AAT AAC GGC AAC GGG TTG GGA GAA TTA GAG GAG	1098
Ser Pro Thr Asp Pro Asn Asn Gly Asn Gly Leu Gly Glu Leu Glu Glu	
120 125 130	
GCA ATG GAA GGG ATC GAG GGC GAT TTC TGG CTC GAC TCT CTG GAC GGT	1146
Ala Met Glu Gly Ile Glu Gly Asp Phe Trp Leu Asp Ser Leu Asp Gly	
135 140 145 150	
GAC CGC TTC GAG GAC GAG AGC CGT ACC ATG CAG AGC GAG AAT ATG CGT	1194
Asp Arg Phe Glu Asp Glu Ser Arg Thr Met Gln Ser Glu Asn Met Arg	
155 160 165	
TTC GTG ATC GAG AAA GAA CTG TTA TCC TGG CTG TCC CGA CAC CTG CCG	1242
Phe Val Ile Glu Lys Glu Leu Leu Ser Trp Leu Ser Arg His Leu Pro	
170 175 180	
GCC GAC CTC GCG TCC GCC GAG CGA GAG ACC TCC CGG TCT CTC CTG GCG	1290
Ala Asp Leu Ala Ser Ala Glu Arg Glu Thr Ser Arg Ser Leu Leu Ala	
185 190 195	
GCC GGG CAC TGG TGC TGC TTG TGG CAC CCT CGG CCG TGC CGC GAA GCG	1338
Ala Gly His Trp Cys Cys Leu Trp His Pro Arg Pro Cys Arg Glu Ala	
200 205 210	
TGT TTG TAC GAC TCG ATT TAC GTG CAG AGT CTT TTC TGC GTC GGG ACG	1386
Cys Leu Tyr Asp Ser Ile Tyr Val Gln Ser Leu Phe Cys Val Gly Thr	
215 220 225 230	
GGG AGA GTC CCG CAA TCG GAG ATG CGC CGT CGC GAA TAC CTG GCC GCC	1434
Gly Arg Val Pro Gln Ser Glu Met Arg Arg Arg Glu Tyr Leu Ala Ala	
235 240 245	
TTG CGC GCC GGC GCG GCT GCC GCC AAC TCT CCC GAA GTG AGC GCC TCG	1482
Leu Arg Ala Gly Ala Ala Ala Ala Asn Ser Pro Glu Val Ser Ala Ser	
250 255 260	
ATC TTT GCG AGG GAC GCT GGA ATC GCG CTG GCG CTG GCG CGG CGC CGT	1530
Ile Phe Ala Arg Asp Ala Gly Ile Ala Leu Ala Leu Ala Arg Arg Arg	
265 270 275	
TGA CGGGAGAATG ACGCCCTCTA GCGGCTTCCT TACCTCCGCG TCCCTGACAA	1583
CCTCGCGGGT TTTTACACTG TCCTCCGTCC ACTCTCCCC CTCACCCACT CCGCGGCAGC	1643
GAAACACAAC CCCCCCCCCC CCCAGAAAC GAGCGACACG CGAGCGCTGC GAAATAATA	1703
AAGTAATATT ATTGTGTGTT TTTACGTTG TTGCAATCGA GAGGCCGTTT GTCTGTCTGT	1763
GTCTGTGCGG AGCTAGGCTT TCCCGGGCGG CCCGTTCCA CCGTTCGGTT AGGCCGGTGG	1823
CGACGGGACA TAGAGAAAGA TAGAGCGCGC GCCCTGGCGG CGAGAGGGTG TTGCGGGGGT	1883
AAATGGGACC CTGAGCTCAC CATTTTGGCG GGGGATTGCA CGGGTAACAA AAAGCTCTCT	1943

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CGCACATAAT GATTTCCCTT AACAGTGGC TGTAAGAGCT TTCTTCGACT GGGACGCGCA 2003
 CGTCCGGAGA CATGATCTTA TCGGTAGCTA CACAGTTCAT GAGGTGGGCC ACGAACGCGC 2063
 GGATCGAGTT TTGGGAACCT TCGGGGAGGT CTTCCGGGAG GGTGAAGTTT GACAGAGGCA 2123
 GCGCTATCAC CAGGAGGCTC CGCACCATCT CCATGCCTAT CCTTATCGCC GCGAGTCCGG 2183
 CGGCCGGCGC GCTGCTCTGG TTATTCCAGT GCGCGGACCG CGAGTGCGCC CCTCCCCGGG 2243
 CTCTGATATA GAGCACCGGC AGCTCGACGG CGGCGGAGAA AAAAGAAAGA ATGTCCGGCC 2303
 CAATGACTGG AACTTTGGGC ACGTCTCTTA TTTCCACGC GCGGCCCCGG GGAATCTGCT 2363
 TGCCCCAGAC CTTGCTTTCC AACTCCCCGT TCGGCCCCC AACTAACTCC GACAGCGCGG 2423
 TCCACAGTCC TACCGCCGCT GCGACGGCGC GCTTAGCCGC GGGCGCTATT CGCGGGTCGT 2483
 GCGCCGTGAT ATCTTCGGCG ACCTGCAGAC TGCCAGCCT TTCCTTCCCT TCAAATACG 2543
 CGCGGGCGGC CTGTACGATC ACCGCGGCCA GATCGGGCCA AAAGAAAATA TCGCAACTCT 2603
 GCGACGCCCC CCAGAATCTC CCTCCGGGCA GGTCCGTGCC CCTAAAGGCC GCCGAGAAAG 2663
 CTAAGTCCAA ATGTGACGTC GGAGGTCTCG ACATGGTCGC CAACCCTCCA AATGCTACCC 2723
 GCCGGCCCCAC GCAACGCGGG CTTTTATAAA GATGGCGCGC GAGACAATAA CACTTACTCA 2783
 TCCGCGTACG CGTTTATTAT TGTCAATATT TGTGTGGTTA TTATTACTGC TACCGCCCTT 2843
 GTTTCTGCAA GGCCCTCGCC GCGGCCCAGG CCACTATTCC GGCAGCGGCC GCCGACGCGG 2903
 CGAGCGTCGC CGCTAACGTC GCGCCGCGG GGAGCGGGGT TTCTTCGACT TAAATAGACT 2963
 CCCGAGAAAA AATTTTGGCT GCCGTTCCGC ATCATCCGAG TCGGAAACAC AGTATGCGGC 3023
 CGAGTTAGGT TTTACTTTTA AAAACTTTAC CGTGCTGTAC GGCCAGGGCG TTCTCAGGCT 3083
 CGAAGGGGCA AGAGTTGTCC AGACTGATGG GTGACTCAGA GACAGCGTTG TCTTGTCTCC 3143
 GTTTACCAA AATATTTCCA CTCCTCTCTC AAAATTTTTTA CCTCCGGTTT CGGTAATTAG 3203
 GAAAGTTTTT GCGCAGGGA GGTTTAAAGC TGCCATGCAT ATGTCAGCGG TACCCAGCAC 3263
 CCACAAATGG AACTCTTTTG CGGCATACGC GCCAGATGAC AAATGGTAAA ACCCTGCGTC 3323
 CAAGCCGCTC CACTCGGGAC TTACTIONAGG CGGGTCGCCC CCCTCACCAG ACCGAATCAC 3383
 GGGTCTGCAC ATCCTGGGAA GGGAAAACAG CTCCCCGGAA ACTTCGTACA GAGATGCCGG 3443
 GCGCACGATT ACCGATAATG TACTCGGACG ATCGTAACTC GCCATAGTTT TCACTGCGTG 3503
 AACCAATTCT TTCCATCCAG AATCCGAGAG CTCAAATCTA GAATTAGGTA GTTTGTAGTG 3563
 CGAATCGACC GCAGAAACTA TAGTCACTTT TACAGGCGCC ATCGCCGCTCAG 3615
 ACTCCACCCC GCTATGATGT CAGAAATATA ACGCTCTTAT TCTAGCAGAG TCAGGCCAAT 3675
 ATATACAGCT TAGAGAAG ATG CGG TTT CGG CGC ATC TGT TCA CGC TCT AGG 3726
 Met Arg Phe Arg Arg Ile Cys Ser Arg Ser Arg
 1 5 10
 GCA GAA AAA CGA AGA AGA ACA ACC GAG AAT CCG CTT ACC TCA AAA CGC 3774
 Ala Glu Lys Arg Arg Arg Thr Thr Glu Asn Pro Leu Thr Ser Lys Arg
 15 20 25

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GTT TGC GTA TTG GAT AGT TTC TCA CGG ACA ATG TCA TTG CGC CCC TAT	3822
Val Cys Val Leu Asp Ser Phe Ser Arg Thr Met Ser Leu Arg Pro Tyr	
30 35 40	
GCA GAA ATT TTG CCG ACC GCG GAA GGC GTC GAG CGC CTC GCC GAA CTT	3870
Ala Glu Ile Leu Pro Thr Ala Glu Gly Val Glu Arg Leu Ala Glu Leu	
45 50 55	
GTT AGT GTG ACA ATG ACA GAA CGC GCG GAA CCT GTG ACA GAG AAT ACA	3918
Val Ser Val Thr Met Thr Glu Arg Ala Glu Pro Val Thr Glu Asn Thr	
60 65 70 75	
GCT GTA AAC AGT ATC CCC CCG GCT AAC GAG AAC GGG CAG AAC TTC GCA	3966
Ala Val Asn Ser Ile Pro Pro Ala Asn Glu Asn Gly Gln Asn Phe Ala	
80 85 90	
TAT GCA GGC GAT GGG CCC TCG ACT ACT GAA AAA GTT GAC GGC TCG CAT	4014
Tyr Ala Gly Asp Gly Pro Ser Thr Thr Glu Lys Val Asp Gly Ser His	
95 100 105	
ACA GAC TTC GAT GAA GCA TCG AGC GAC TAC GCC GGC CCT GTC CCG CTC	4062
Thr Asp Phe Asp Glu Ala Ser Ser Asp Tyr Ala Gly Pro Val Pro Leu	
110 115 120	
GCG CAA ACT AGA TTG AAG CAT TCG GAT GAA TTT CTT CAG CAC TTC CGA	4110
Ala Gln Thr Arg Leu Lys His Ser Asp Glu Phe Leu Gln His Phe Arg	
125 130 135	
GTT TTA GAC GAT TTG GTG GAG GGG GCT TAC GGG TTT ATC TGC GAC GTC	4158
Val Leu Asp Asp Leu Val Glu Gly Ala Tyr Gly Phe Ile Cys Asp Val	
140 145 150 155	
CGT CGC TAC ACC GAG GAA GAG CAA CGT CGA AGA GGG GTT AAC AGT ACT	4206
Arg Arg Tyr Thr Glu Glu Glu Gln Arg Arg Arg Gly Val Asn Ser Thr	
160 165 170	
AAC CAG GGG AAA TCA AAA TGT AAG CGC CTG ATA GCT AAA TAT GTG AAA	4254
Asn Gln Gly Lys Ser Lys Cys Lys Arg Leu Ile Ala Lys Tyr Val Lys	
175 180 185	
AAT GGA ACA AGG GCG GCC TCT CAG CTG GAA AAT GAA ATT TTG GTT CTC	4302
Asn Gly Thr Arg Ala Ala Ser Gln Leu Glu Asn Glu Ile Leu Val Leu	
190 195 200	
GGG CGC CTA AAT CAC GAG AAT GTT CTC AAG ATC CAG GAA ATC CTT CGG	4350
Gly Arg Leu Asn His Glu Asn Val Leu Lys Ile Gln Glu Ile Leu Arg	
205 210 215	
TAC CCG GAT AAT ACG TAC ATG TTA ACG CAG AGG TAT CAG TTC GAC TTG	4398
Tyr Pro Asp Asn Thr Tyr Met Leu Thr Gln Arg Tyr Gln Phe Asp Leu	
220 225 230 235	
TAC AGC TAC ATG TAC GAT GAA GCG TTC GAC TGG AAA GAC AGT CCA ATG	4446
Tyr Ser Tyr Met Tyr Asp Glu Ala Phe Asp Trp Lys Asp Ser Pro Met	
240 245 250	
CTT AAA CAG ACT AGA CGC ATC ATG AAG CAG CTC ATG TCA GCG GTC TCG	4494
Leu Lys Gln Thr Arg Arg Ile Met Lys Gln Leu Met Ser Ala Val Ser	
255 260 265	
TAT ATC CAT TCA AAG AAA CTG ATT CAC AGG GAC ATC AAA CTC GAA AAT	4542
Tyr Ile His Ser Lys Lys Leu Ile His Arg Asp Ile Lys Leu Glu Asn	
270 275 280	
ATT TTC TTA AAC TGC GAC GGC AAG ACA GTG CTG GGC GAC TTT GGA ACT	4590
Ile Phe Leu Asn Cys Asp Gly Lys Thr Val Leu Gly Asp Phe Gly Thr	
285 290 295	

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GTC ACG CCT TTT GAA AAT GAG CGG GAG CCC TTC GAA TAT GGA TGG GTG Val Thr Pro Phe Glu Asn Glu Arg Glu Pro Phe Glu Tyr Gly Trp Val 300 305 310 315	4638
GGG ACC GTG GCT ACT AAC TCT CCC GAG ATA CTC GCC AGG GAT TCG TAC Gly Thr Val Ala Thr Asn Ser Pro Glu Ile Leu Ala Arg Asp Ser Tyr 320 325 330	4686
TGT GAA ATT ACA GAC ATT TGG AGC TGC GGA GTA GTA TTG CTG GAA ATG Cys Glu Ile Thr Asp Ile Trp Ser Cys Gly Val Val Leu Leu Glu Met 335 340 345	4734
GTA AGC CAT GAA TTT TGC CCG ATC GGC GAT GGC GGG GGA AAT CCG CAC Val Ser His Glu Phe Cys Pro Ile Gly Asp Gly Gly Gly Asn Pro His 350 355 360	4782
CAG CAA TTG CTG AAA GTT ATC GAC TCT CTC TCA GTT TGT GAT GAA GAG Gln Gln Leu Leu Lys Val Ile Asp Ser Leu Ser Val Cys Asp Glu Glu 365 370 375	4830
TTC CCA GAC CCC CCG TGT AAT CTG TAC AAT TAT TTG CAT TAT GCG AGC Phe Pro Asp Pro Pro Cys Asn Leu Tyr Asn Tyr Leu His Tyr Ala Ser 380 385 390 395	4878
ATC GAT CGC GCC GGA CAT ACG GTC CCG TCG CTC ATA CGG AAC CTC CAC Ile Asp Arg Ala Gly His Thr Val Pro Ser Leu Ile Arg Asn Leu His 400 405 410	4926
CTT CCG GCG GAT GTG GAA TAC CCT CTA GTT AAA ATG CTT ACT TTT GAC Leu Pro Ala Asp Val Glu Tyr Pro Leu Val Lys Met Leu Thr Phe Asp 415 420 425	4974
TGG CGT TTG AGA CCC AGC GCG GCC GAA GTA TTG GCA ATG CCA CTG TTT Trp Arg Leu Arg Pro Ser Ala Ala Glu Val Leu Ala Met Pro Leu Phe 430 435 440	5022
TCG GCT GAA GAG GAA CGG ACC ATA ACA ATT ATT CAT GGA AAA CAT AAA Ser Ala Glu Glu Glu Arg Thr Ile Thr Ile Ile His Gly Lys His Lys 445 450 455	5070
CCC ATC CGA CCC GAA ATC CGT GCG CGG GTG CCA CGG TCC ATG AGT GAA Pro Ile Arg Pro Glu Ile Arg Ala Arg Val Pro Arg Ser Met Ser Glu 460 465 470 475	5118
GGT TAA TAATAAAGGA CGGAGATAGA GAACTGAAGC GTCAGATTTT TTTAAAAAAA Gly .	5174
TAAATGATCG AGAACTTATG ATTTGTCTTT CTTGA ATG ACC TTG CCC CAT CGA Met Thr Leu Pro His Arg 1 5	5227
TTA ACG AAA AGA CCT TTC GCG CGT CGA TTC TGC TCG GTC TTT GTG ATA Leu Thr Lys Arg Pro Phe Ala Arg Arg Phe Cys Ser Val Phe Val Ile 10 15 20	5275
CAT TAT AGT GAG ACT AAA CTC GAC CGA TAT AAC AAG ACA ATG TTA CTC His Tyr Ser Glu Thr Lys Leu Asp Arg Tyr Asn Lys Thr Met Leu Leu 25 30 35	5323
TAT AGA CCG GAC TCA ACC ATG CGG CAT AGC GGA GGC GAC GCA AAT CAC Tyr Arg Pro Asp Ser Thr Met Arg His Ser Gly Asp Ala Asn His 40 45 50	5371
AGA GGG ATA AGG CCG AGG CGG AAA TCT ATT GGA GCG TTT AGC GCG CGC Arg Gly Ile Arg Pro Arg Arg Lys Ser Ile Gly Ala Phe Ser Ala Arg 55 60 65 70	5419

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GAA AAG ACT GGA AAA CGA AAT GCG CTG ACG GAA AGC AGC TCC TCC TCC	5467
Glu Lys Thr Gly Lys Arg Asn Ala Leu Thr Glu Ser Ser Ser Ser Ser	
75 80 85	
GAC ATG CTA GAT CCG TTT TCC ACG GAT AAG GAA TTT GGC GGT AAG TGG	5515
Asp Met Leu Asp Pro Phe Ser Thr Asp Lys Glu Phe Gly Gly Lys Trp	
90 95 100	
ACG GTA GAC GGA CCT GCC GAC ATT ACT GCC GAG GTC CTT TCT CAG GCA	5563
Thr Val Asp Gly Pro Ala Asp Ile Thr Ala Glu Val Leu Ser Gln Ala	
105 110 115	
TGG GAC GTT CTC CAA TTA GTG AAG CAT GAA GAT GCG GAG GAG GAG AGA	5611
Trp Asp Val Leu Gln Leu Val Lys His Glu Asp Ala Glu Glu Glu Arg	
120 125 130	
GTG ACT TAT GAG TCC AAA CCG ACC CCG ATA CAG CCG TTC AAT GCC TGG	5659
Val Thr Tyr Glu Ser Lys Pro Thr Pro Ile Gln Pro Phe Asn Ala Trp	
135 140 145 150	
CCG GAC GGG CCG AGT TGG AAC GCG CAG GAT TTT ACT CGA GCG CCA ATA	5707
Pro Asp Gly Pro Ser Trp Asn Ala Gln Asp Phe Thr Arg Ala Pro Ile	
155 160 165	
GTT TAT CCC TCT GCG GAG GTA TTG GAC GCA GAG GCG TTG AAA GTA GGG	5755
Val Tyr Pro Ser Ala Glu Val Leu Asp Ala Glu Ala Leu Lys Val Gly	
170 175 180	
GCA TTC GTT AGC CGA GTT TTA CAA TGT GTA CCG TTC ACG CGA TCA AAG	5803
Ala Phe Val Ser Arg Val Leu Gln Cys Val Pro Phe Thr Arg Ser Lys	
185 190 195	
AAA AGC GTT ACG GTG CGG GAT GCG CAG TCG TTT TTG GGG GAC TCG TTC	5851
Lys Ser Val Thr Val Arg Asp Ala Gln Ser Phe Leu Gly Asp Ser Phe	
200 205 210	
TGG AGA ATA ATG CAG AAC GTT TAC ACG GTT GTC TTA CGA CAG CAC ATA	5899
Trp Arg Ile Met Gln Asn Val Tyr Thr Val Val Leu Arg Gln His Ile	
215 220 225 230	
ACT CGA CTC AGG CAC CCT TCC AGC AAA AGC ATT GTT AAC TGC AAC GAC	5947
Thr Arg Leu Arg His Pro Ser Ser Lys Ser Ile Val Asn Cys Asn Asp	
235 240 245	
CCT CTA TGG TAC GCC TAC GCG AAT CAA TTT CAC TGG AGA GGA ATG CGC	5995
Pro Leu Trp Tyr Ala Tyr Ala Asn Gln Phe His Trp Arg Gly Met Arg	
250 255 260	
GTG CCG TCG CTT AAA TTA GCC TCT CCC CCG GAG GAG AAT ATT CAA CAC	6043
Val Pro Ser Leu Lys Leu Ala Ser Pro Pro Glu Glu Asn Ile Gln His	
265 270 275	
GGC CCA ATG GCC GCC GTT TTT AGA AAC GCG GGG GCT GGT CTG TTC CTG	6091
Gly Pro Met Ala Ala Val Phe Arg Asn Ala Gly Ala Gly Leu Phe Leu	
280 285 290	
TGG CCT GCC ATG CGC GCA GCC TTT GAA GAG CGC GAC AAG CGA CTG TTA	6139
Trp Pro Ala Met Arg Ala Ala Phe Glu Glu Arg Asp Lys Arg Leu Leu	
295 300 305 310	
AGA GCA TGC CTG TCT TCA CTC GAT ATC ATG GAC GCA GCC GTC CTC GCG	6187
Arg Ala Cys Leu Ser Ser Leu Asp Ile Met Asp Ala Ala Val Leu Ala	
315 320 325	
TCG TTT CCA TTT TAC TGG CGC GGC GTC CAA GAC ACC TCG CGC TTC GAG	6235
Ser Phe Pro Phe Tyr Trp Arg Gly Val Gln Asp Thr Ser Arg Phe Glu	
330 335 340	

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CCT Pro	CGC Ala	CTG Leu	GGC Gly	TGT Cys	TGT Leu	TCA Ser	GAG Glu	TAC Tyr	TTT Phe	GCA Ala	CTA Leu	GTG Val	GTG Val	TTA Leu	CTG Leu	6283		
345																350	355	
GCC Ala	GAG Glu	ACG Thr	GTC Val	TTA Leu	GCG Ala	ACC Thr	ATG Met	TTC Phe	GAC Asp	CAC His	GCA Ala	CTG Leu	GTA Val	TTC Phe	ATG Met	6331		
360																365	370	
AGG Arg	GCG Ala	CTG Leu	GCA Ala	GAC Asp	GGC Gly	AAT Asn	TTC Phe	GAT Asp	GAC Asp	TAT Tyr	GAC Asp	GAA Glu	ACT Thr	AGA Arg	TAT Tyr	6379		
375																380	385	390
ATA Ile	GAC Asp	CCC Pro	GTT Val	AAA Lys	AAC Asn	GAG Glu	TAC Tyr	CTG Leu	AAC Asn	GGA Gly	GCC Ala	GAG Glu	GGT Gly	ACT Thr	CTG Leu	6427		
395																400	405	
TTA Leu	CGG Arg	GGC Gly	ATA Ile	GTG Val	GCC Ala	TCC Ser	AAC Asn	ACC Thr	GCT Ala	CTG Leu	GCG Ala	GTG Val	GTT Val	TGC Cys	GCA Ala	6475		
410																415	420	
AAC Asn	ACC Thr	TAT Tyr	TCG Ser	ACG Thr	ATA Ile	AGA Arg	AAA Lys	CTC Leu	CCG Pro	TCC Ser	GTG Val	GCA Ala	ACT Thr	AGC Ser	GCG Ala	6523		
425																430	435	
TGC Cys	AAT Asn	GTT Val	GCC Ala	TAC Tyr	AGG Arg	ACC Thr	GAA Glu	ACG Thr	CTG Leu	AAA Lys	GCG Ala	AGG Arg	CGC Arg	CCT Pro	GGC Gly	6571		
440																445	450	
ATG Met	AGC Ser	GAC Asp	ATA Ile	TAC Tyr	CGG Arg	ATA Ile	TTA Leu	CAA Gln	AAA Lys	GAG Glu	TTT Phe	TTC Phe	TTT Phe	TAC Tyr	ATT Ile	6619		
455																460	465	470
GCG Ala	TGG Trp	CTC Leu	CAG Gln	AGG Arg	GTT Val	GCA Ala	ACA Thr	CAC His	GCA Ala	AAT Asn	TTC Phe	TGT Cys	TTA Leu	AAC Asn	ATT Ile	6667		
475																480	485	
CTG Leu	AAG Lys	AGA Arg	AGC Ser	GTG Val	GAT Asp	ACG Thr	GGG Gly	GCC Ala	CCG Pro	CCA Pro	TTT Phe	TTG Leu	TTC Phe	AGG Arg	GCC Ala	6715		
490																495	500	
AGC Ser	TCG Ser	GAG Glu	AAG Lys	CGG Arg	CTG Leu	CAG Gln	CAG Gln	TTA Leu	AAT Asn	AAA Lys	ATG Met	CTC Leu	TGC Cys	CCC Pro	CTT Leu	6763		
505																510	515	
CTC Leu	GTG Val	CCG Pro	ATT Ile	CAA Gln	TAT Tyr	GAA Glu	GAC Asp	TTT Phe	TCG Ser	AAG Lys	GCC Ala	ATG Met	GGG Gly	TCT Ser	GAG Glu	6811		
520																525	530	
CTC Leu	AAG Lys	AGG Arg	GAA Glu	AAG Lys	TTA Leu	GAG Glu	ACA Thr	TTC Phe	GTT Val	AAA Lys	GCT Ala	ATT Ile	TCC Ser	AGC Ser	GAC Asp	6859		
535																540	545	550
AGG Arg	GAC Asp	CCG Pro	AGG Arg	GGG Gly	TCC Ser	TTA Leu	AGA Arg	TTT Phe	CTC Leu	ATT Ile	TCG Ser	GAC Asp	CAT His	GCA Ala	AGG Arg	6907		
555																560	565	
GAA Glu	ATT Ile	ATT Ile	GCA Ala	GAC Asp	GGA Gly	GTA Val	CGG Arg	TTT Phe	AAG Lys	CCG Pro	GTG Val	ATA Ile	GAC Asp	GAG Glu	CCG Pro	6955		
570																575	580	
GTT Val	CGG Arg	GCT Ala	TCA Ser	GTT Val	GCG Ala	CTG Leu	AGT Ser	ACC Thr	GCT Ala	GCC Ala	GCT Ala	GGG Gly	AAA Lys	GTG Val	AAA Lys	7003		
585																590	595	
GCG Ala	CGA Arg	CGC Arg	TTA Leu	ACC Thr	TCA Ser	GTT Val	CGC Arg	GCG Ala	CCC Pro	GTA Val	CCG Pro	GGC Gly	GCA Ala	GGC Gly	GCC Ala	7051		
600																605	610	

GTT TCC GCG CGC CGG AAA TCG GAA ATA TGA TAAAAATGCT TGGCATTGCT	7101
Val Ser Ala Arg Lys Ser Glu Ile .	
615 620	
GGGCGAAGAG GCGTGATCTG AAGGGCTCCA CAATGACGTA ACTGAGCTAC GCATCCCTAT	7161
AAAGTGTACC CGCTGACCGC TAGCCCATAC AGTGTTACAG GAGGGGAGAG AGACAACTTC	7221
AGCTCGAAGT CTGAAGAGAC ATC ATG AGC GGC TTC AGT AAC ATA GGA TCG	7271
Met Ser Gly Phe Ser Asn Ile Gly Ser	
1 5	
ATT GCC ACC GTT TCC CTA GTA TGC TCG CTT TTG TGC GCA TCT GTA TTA	7319
Ile Ala Thr Val Ser Leu Val Cys Ser Leu Leu Cys Ala Ser Val Leu	
10 15 20 25	
GGG GCG CCG GTA CTG GAC GGG CTC GAG TCG AGC CCT TTC CCG TTC GGG	7367
Gly Ala Pro Val Leu Asp Gly Leu Glu Ser Ser Pro Phe Pro Phe Gly	
30 35 40	
GGC AAA ATT ATA GCC CAG GCG TGC AAC CGC ACC ACG ATT GAG GTG ACG	7415
Gly Lys Ile Ile Ala Gln Ala Cys Asn Arg Thr Thr Ile Glu Val Thr	
45 50 55	
GTC CCG TGG AGC GAC TAC TCT GGT CGC ACC GAA GGA GTG TCA GTC GAG	7463
Val Pro Trp Ser Asp Tyr Ser Gly Arg Thr Glu Gly Val Ser Val Glu	
60 65 70	
GTG AAA TGG TTC TAC GGG AAT AGT AAT CCC GAA AGC TTC GTG TTC GGG	7511
Val Lys Trp Phe Tyr Gly Asn Ser Asn Pro Glu Ser Phe Val Phe Gly	
75 80 85	
GTG GAT AGC GAA ACG GGC AGT GGA CAC GAG GAC CTG TCT ACG TGC TGG	7559
Val Asp Ser Glu Thr Gly Ser Gly His Glu Asp Leu Ser Thr Cys Trp	
90 95 100 105	
GCT CTA ATC CAT AAT CTG AAC GCG TCT GTG TGC AGG GCG TCT GAC GCC	7607
Ala Leu Ile His Asn Leu Asn Ala Ser Val Cys Arg Ala Ser Asp Ala	
110 115 120	
GGG ATA CCT GAT TTC GAC AAG CAG TGC GAA AAA GTG CAG AGA AGA CTG	7655
Gly Ile Pro Asp Phe Asp Lys Gln Cys Glu Lys Val Gln Arg Arg Leu	
125 130 135	
CGC TCC GGG GTG GAA CTT GGT AGT TAC GTG TCT GGC AAT GGA TCC CTG	7703
Arg Ser Gly Val Glu Leu Gly Ser Tyr Val Ser Gly Asn Gly Ser Leu	
140 145 150	
GTG CTG TAC CCA GGG ATG TAC GAT GCC GGC ATC TAC GCC TAC CAG CTC	7751
Val Leu Tyr Pro Gly Met Tyr Asp Ala Gly Ile Tyr Ala Tyr Gln Leu	
155 160 165	
TCA GTG GGT GGG AAG GGA TAT ACC GGG TCT GTT TAT CTA GAC GTC GGA	7799
Ser Val Gly Gly Lys Gly Tyr Thr Gly Ser Val Tyr Leu Asp Val Gly	
170 175 180 185	
CCA AAC CCC GGA TGC CAC GAC CAG TAT GGG TAC ACC TAT TAC AGC CTG	7847
Pro Asn Pro Gly Cys His Asp Gln Tyr Gly Tyr Thr Tyr Tyr Ser Leu	
190 195 200	
GCC GAC GAG GCG TCA GAC TTA TCA TCT TAT GAC GTA GCC TCG CCC GAA	7895
Ala Asp Glu Ala Ser Asp Leu Ser Ser Tyr Asp Val Ala Ser Pro Glu	
205 210 215	
CTC GAC GGT CCT ATG GAG GAA GAT TAT TCC AAT TGT CTA GAC ATG CCC	7943
Leu Asp Gly Pro Met Glu Glu Asp Tyr Ser Asn Cys Leu Asp Met Pro	
220 225 230	

CCG CTA CGC CCA TGG ACA ACC GTT TGT TCG CAT GAC GTC GAG GAG CAG	7991
Pro Leu Arg Pro Trp Thr Thr Val Cys Ser His Asp Val Glu Glu Gln	
235 240 245	
GAA AAC GCC ACG GAC GAG CTT TAC CTA TGG GAC GAG GAA TGC GCC GGT	8039
Glu Asn Ala Thr Asp Glu Leu Tyr Leu Trp Asp Glu Glu Cys Ala Gly	
250 255 260 265	
CCG CTG GAC GAG TAC GTC GAC GAA AGG TCA GAG ACG ATG CCC AGG ATG	8087
Pro Leu Asp Glu Tyr Val Asp Glu Arg Ser Glu Thr Met Pro Arg Met	
270 275 280	
GTT GTC TTT TCA CCG CCC TCT ACG CTC CAG CAG TAG CCACCCGAGA	8133
Val Val Phe Ser Pro Pro Ser Thr Leu Gln Gln .	
285 290	
GTGTTTTTTTG TGAGCGCCCCA CGCAACATAC CTAACGTGCTT CATTTCTGAT CAATTATTGC	8193
GTATTGAATA AATAAACAGT ACAAAGCAT CAGGTGTGGT TTGCGTGTCT GTGCTAAACC	8253
ATGGCGTGTG CGGGTGAAAC CGTAAATTAC GTGATAATAA ATAGCATAGG AGTTGGCGTG	8313
CAGCGTATTT CGCCGAGAGA TGGGGACAAT GTTAGTGTG CGCCTTTTCC TACTTGCACT	8373
AGCGGACGCG GCGTTGCCGA CCGGCAGATT CTGCCGAGTT TGGAAGGTGC CTCCGGGAGG	8433
AACCATCCAA GAGAACCTGG CGGTGCTCGC GGAATCGCCG GTCACGGGAC ACGCGACATA	8493
TCCGCCGCCT GAAGGCGCCG TCAGCTTTCA GATTTTTGCG GACACCCCTA CTTTGCGCAT	8553
TCGCTACGGC GCTACGGAGG ACGAACTTGC ACTGGAGCGC GGGACGTCCG CCTCAGACGC	8613
GGACAACGTG ACATTTTCGC TGTCATATCG CCCGCGCCCA GAAATTCACG GAGCATACTT	8673
CACCATAGGG GTATTGCTA CTGGCCAGAG CACGGAAAGC AGCTATTTCG TCATCAGTCG	8733
GGTCTTAGTT AACGCCTCTC TGGAACGGTC CGTGCGCCTG GAAACGCCGT GCGATGAAAA	8793
TTTTTTGCAG AACGAGCCTA CATGGGGCTC GAAGCGTTGG TTAGGCCCC CGTCGCCTTA	8853
TGTGCGAGAT AACGATGTCG CCGTGTGAC AAAAGCGCAG TACATTGGGG AGTGCTACTC	8913
CAACTCGGCG GCCCAGACGG GGCTCACGTC TCTCAACATG ACCTTTTTCT ATTCGCCTAA	8973
AAGAATAGTA AACGTCACGT GGACAACCGG CGGCCCTCC CCCTCGCGCA TAACGGTATA	9033
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CAGCACTAGC GATATGGGAT TCTTCTCCAC GGCACGTGCT ACCGGATCAG AAACCTCTTC	9513
GGTACCCGTC CAGGAAACGG ATAGAACTCT TTCGACAACT CCTCTTACCC TTCCACTGAC	9573
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ACTAGGGTAT	CAAGAGGCTG	CGACGTTGTC	GAGCTCAACC	CGATTTCTAA	CGTGGACGAC	11490
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GAGGACACCG	AGCACGATGA	TCCAAACTCG	GATCCTGACT	ATTACAATGA	CATGCCCGCC	12270										
GTGATCCCGG	TGGAGGAGAC	TACTAAAAGT	TCTAATGCCG	TCTCCATGCC	CATATTGCGG	12330										
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GAAAAGC	ATG	GCA	TCG	CTA	CTT	GGA	ACT	CTG	GCT	CTC	CTT	GCC	GCG	ACG	12551	
	Met	Ala	Ser	Leu	Leu	Gly	Thr	Leu	Ala	Leu	Leu	Ala	Ala	Thr		
	1					5						10				
CTC	GCA	CCC	TTC	GGC	GCG	ATG	GGA	ATC	GTG	ATC	ACT	GGA	AAT	CAC	GTC	12599
Leu	Ala	Pro	Phe	Gly	Ala	Met	Gly	Ile	Val	Ile	Thr	Gly	Asn	His	Val	
15					20					25					30	
TCC	GCC	AGG	ATT	GAC	GAC	GAT	CAC	ATC	GTG	ATC	GTC	GCG	CCT	CGC	CCC	12647
Ser	Ala	Arg	Ile	Asp	Asp	Asp	His	Ile	Val	Ile	Val	Ala	Pro	Arg	Pro	
				35					40					45		
GAA	GCT	ACA	ATT	CAA	CTG	CAG	CTA	TTT	TTC	ATG	CCT	GGC	CAG	AGA	CCC	12695
Glu	Ala	Thr	Ile	Gln	Leu	Gln	Leu	Phe	Phe	Met	Pro	Gly	Gln	Arg	Pro	
			50					55					60			
CAC	AAA	CCC	TAC	TCA	GGA	ACC	GTC	CGC	GTC	GCG	TTT	CGG	TCT	GAT	ATA	12743
His	Lys	Pro	Tyr	Ser	Gly	Thr	Val	Arg	Val	Ala	Phe	Arg	Ser	Asp	Ile	
		65					70					75				
ACA	AAC	CAG	TGC	TAC	CAG	GAA	CTT	AGC	GAG	GAG	CGC	TTT	GAA	AAT	TGC	12791
Thr	Asn	Gln	Cys	Tyr	Gln	Glu	Leu	Ser	Glu	Glu	Arg	Phe	Glu	Asn	Cys	
	80						85				90					
ACT	CAT	CGA	TCG	TCT	TCT	GTT	TTT	GTC	GGC	TGT	AAA	GTG	ACC	GAG	TAC	12839
Thr	His	Arg	Ser	Ser	Ser	Val	Phe	Val	Gly	Cys	Lys	Val	Thr	Glu	Tyr	
	95				100					105					110	
ACG	TTC	TCC	GCC	TCG	AAC	AGA	CTA	ACC	GGA	CCT	CCA	CAC	CCG	TTT	AAG	12887
Thr	Phe	Ser	Ala	Ser	Asn	Arg	Leu	Thr	Gly	Pro	Pro	His	Pro	Phe	Lys	
				115					120					125		
CTC	ACT	ATA	CGA	AAT	CCT	CGT	CCG	AAC	GAC	AGC	GGG	ATG	TTC	TAC	GTA	12935
Leu	Thr	Ile	Arg	Asn	Pro	Arg	Pro	Asn	Asp	Ser	Gly	Met	Phe	Tyr	Val	
			130					135					140			
ATT	GTT	CGG	CTA	GAC	GAC	ACC	AAA	GAA	CCC	ATT	GAC	GTC	TTC	GCG	ATC	12983
Ile	Val	Arg	Leu	Asp	Asp	Thr	Lys	Glu	Pro	Ile	Asp	Val	Phe	Ala	Ile	
		145					150					155				

CAA CTA TCG GTG TAT CAA TTC GCG AAC ACC GCC GCG ACT CGC GGA CTC Gln Leu Ser Val Tyr Gln Phe Ala Asn Thr Ala Ala Thr Arg Gly Leu 160 165 170	13031
TAT TCC AAG GCT TCG TGT CGC ACC TTC GGA TTA CCT ACC GTC CAA CTT Tyr Ser Lys Ala Ser Cys Arg Thr Phe Gly Leu Pro Thr Val Gln Leu 175 180 185 190	13079
GAG GCC TAT CTC AGG ACC GAG GAA AGT TGG CGC AAC TGG CAA GCG TAC Glu Ala Tyr Leu Arg Thr Glu Glu Ser Trp Arg Asn Trp Gln Ala Tyr 195 200 205	13127
GTT GCC ACG GAG GCC ACG ACG ACC AGC GCC GAG GCG ACA ACC CCG ACG Val Ala Thr Glu Ala Thr Thr Thr Ser Ala Glu Ala Thr Thr Pro Thr 210 215 220	13175
CCC GTC ACT GCA ACC AGC GCC TCC GAA CTT GAA GCG GAA CAC TTT ACC Pro Val Thr Ala Thr Ser Ala Ser Glu Leu Glu Ala Glu His Phe Thr 225 230 235	13223
TTT CCC TGG CTA GAA AAT GGC GTG GAT CAT TAC GAA CCG ACA CCC GCA Phe Pro Trp Leu Glu Asn Gly Val Asp His Tyr Glu Pro Thr Pro Ala 240 245 250	13271
AAC GAA AAT TCA AAC GTT ACT GTC CGT CTC GGG ACA ATG AGC CCT ACG Asn Glu Asn Ser Asn Val Thr Val Arg Leu Gly Thr Met Ser Pro Thr 255 260 265 270	13319
CTA ATT GGG GTA ACC GTG GCT GCC GTC GTG AGC GCA ACG ATC GGC CTC Leu Ile Gly Val Thr Val Ala Ala Val Val Ser Ala Thr Ile Gly Leu 275 280 285	13367
GTC ATT GTA ATT TCC ATC GTC ACC AGA AAC ATG TGC ACC CCG CAC CGA Val Ile Val Ile Ser Ile Val Thr Arg Asn Met Cys Thr Pro His Arg 290 295 300	13415
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AGG GAA TCG CGA AAA TTT GGA CCC ATG GTT GCG TGC GAA ATA AAC AAG Arg Glu Ser Arg Lys Phe Gly Pro Met Val Ala Cys Glu Ile Asn Lys 320 325 330	13511
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CCG TCT GCG CTA AGC TCG CCC GAC TCA ATA AAA ATG TGA TTAAGTCTGA Pro Ser Ala Leu Ser Ser Pro Asp Ser Ile Lys Met 355 360	13608
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ACTTAGGAGG AGAATTCAGC CGGGGAGAGC CCCTGTTGAG TAGGCTTGGG AGCATATTGC	13788
AGG ATG AAC ATG TTA GTG ATA GTT CTC GCC TCT TGT CTT GCG CGC CTA Met Asn Met Leu Val Ile Val Leu Ala Ser Cys Leu Ala Arg Leu 1 5 10 15	13836
ACT TTT GCG ACG CGA CAC GTC CTC TTT TTG GAA GGC ACT CAG GCT GTC Thr Phe Ala Thr Arg His Val Leu Phe Leu Glu Gly Thr Gln Ala Val 20 25 30	13884

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CTC Leu	GGG Gly	GAA Glu	GAT Asp 35	GAT Asp	CCC Pro	AGA Arg	AAC Asn	GTT Val 40	CCG Pro	GAA Glu	GGG Gly	ACT Thr 45	GTA Val	ATC Ile	AAA Lys	13932
TGG Trp	ACA Thr	AAA Lys 50	GTC Val	CTG Leu	CGG Arg	AAC Asn	GCG Ala 55	TGC Cys	AAG Lys	ATG Met	AAG Lys	GCG Ala 60	GCC Ala	GAT Asp	GTC Val	13980
TGC Cys	TCT Ser 65	TCG Ser	CCT Pro	AAC Asn	TAT Tyr	TGC Cys 70	TTT Phe	CAT His	GAT Asp	TTA Leu	ATT Ile 75	TAC Tyr	GAC Asp	GGA Gly	GGA Gly	14028
AAG Lys 80	AAA Lys	GAC Asp	TGC Cys	CCG Pro	CCC Pro 85	GCG Ala	GGA Gly	CCC Pro	CTG Leu	TCT Ser 90	GCA Ala	AAC Asn	CTG Leu	GTA Val	ATT Ile 95	14076
TTA Leu	CTA Leu	AAG Lys	CGC Arg 100	GGC Gly	GAA Glu	AGC Ser	TTC Phe	GTC Val 105	GTG Val	CTG Leu	GGT Gly	TCT Ser	GGG Gly	CTA Leu 110	CAC His	14124
AAC Asn	AGC Ser	AAT Asn 115	ATA Ile	ACT Thr	AAT Asn	ATC Ile	ATG Met	TGG Trp 120	ACA Thr	GAG Glu	TAC Tyr	GGA Gly 125	GGC Gly	CTG Leu	CTC Leu	14172
TTT Phe	GAT Asp 130	CCT Pro	GTA Val	ACT Thr	CGT Arg	TCG Ser	GAC Asp 135	GAG Glu	GGA Gly	ATC Ile	TAT Tyr	TTT Phe 140	CGA Arg	CGG Arg	ATC Ile	14220
TCT Ser 145	CAG Gln	CCA Pro	GAT Asp	CTG Leu	GCC Ala	ATG Met 150	GAA Glu	ACT Thr	ACA Thr	TCG Ser	TAC Tyr 155	AAC Asn	GTC Val	AGC Ser	GTT Val	14268
CTT Leu 160	TCG Ser	CAC His	GTA Val	GAC Asp	GAG Glu 165	AAG Lys	GCT Ala	CCA Pro	GCA Ala	CCG Pro 170	CAC His	GAG Glu	GTG Val	GAG Glu	ATA Ile 175	14316
GAC Asp	ACC Thr	ATC Ile	AAG Lys 180	CCG Pro	TCA Ser	GAG Glu	GCC Ala	CAC His	GCG Ala 185	CAC His	GTG Val	GAA Glu	TTA Leu	CAA Gln 190	ATG Met	14364
CTG Leu	CCG Pro	TTT Phe 195	CAT His	GAA Glu	CTC Leu	AAC Asn	GAC Asp 200	AAC Asn	AGC Ser	CCC Pro	ACC Thr	TAT Tyr 205	GTG Val	ACC Thr	CCT Pro	14412
GTT Val	CTT Leu 210	AGA Arg	GTC Val	TTC Phe	CCA Pro	CCG Pro 215	ACC Thr	GAG Glu	CAC His	GTA Val	AAA Lys 220	TTT Phe	AAC Asn	GTT Val	ACG Thr	14460
TAT Tyr 225	TCG Ser	TGG Trp	TAT Tyr	GGG Gly	TTT Phe	GAT Asp 230	GTC Val	AAA Lys	GAG Glu	GAG Glu	TGC Cys 235	GAA Glu	GAA Glu	GTG Val	AAA Lys	14508
CTG Leu 240	TTC Phe	GAG Glu	CCG Pro	TGC Cys	GTA Val 245	TAC Tyr	CAT His	CCT Pro	ACA Thr 250	GAC Asp	GGC Gly	AAA Lys	TGT Cys	CAG Gln	TTT Phe 255	14556
CCC Pro	GCA Ala	ACC Thr	AAC Asn 260	CAG Gln	AGA Arg	TGC Cys	CTC Leu	ATA Ile 265	GGA Gly	TCT Ser	GTC Val	TTG Leu	ATG Met	GCG Ala 270	GAA Glu	14604
TTC Phe	TTG Leu	GGC Gly 275	GCG Ala	GCC Ala	TCT Ser	TTG Leu	CTG Leu	GAT Asp 280	TGT Cys	TCC Ser	CGC Arg	GAT Asp 285	ACT Thr	CTA Leu	GAA Glu	14652
GAC Asp	TGC Cys 290	CAC His	GAA Glu	AAT Asn	CGC Arg	GTG Val 295	CCG Pro	AAC Asn 295	CTA Leu	CGG Arg	TTC Phe 300	GAT Asp 300	TCG Ser	CGA Arg	CTC Leu	14700

TCC GAG TCA CGC GCA GGC CTG GTG ATC AGT CCT CTT ATA GCC ATC CCC Ser Glu Ser Arg Ala Gly Leu Val Ile Ser Pro Leu Ile Ala Ile Pro 305 310 315	14748
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TAC ACG GTG CTC GGG AAA CGT AAC AGT CCG CGC GTA GTA GTC GAA ACG Tyr Thr Val Leu Gly Lys Arg Asn Ser Pro Arg Val Val Val Glu Thr 340 345 350	14844
CAC ATG CCC TCG AAG GTC CCG ATG AAC AAA GTA GTA ATT GGC AGT CCC His Met Pro Ser Lys Val Pro Met Asn Lys Val Val Ile Gly Ser Pro 355 360 365	14892
GGA CCA ATG GAC GAA ACG GGT AAC TAT AAA ATG TAC TTC GTC GTC GCG Gly Pro Met Asp Glu Thr Gly Asn Tyr Lys Met Tyr Phe Val Val Ala 370 375 380	14940
GGG GTG GCC GCG ACG TGC GTA ATT CTT ACA TGC GCT CTG CTT GTG GGG Gly Val Ala Ala Thr Cys Val Ile Leu Thr Cys Ala Leu Leu Val Gly 385 390 395	14988
AAA AAG AAG TGC CCC GCG CAC CAA ATG GGT ACT TTT TCC AAG ACC GAA Lys Lys Lys Cys Pro Ala His Gln Met Gly Thr Phe Ser Lys Thr Glu 400 405 410 415	15036
CCA TTG TAC GCG CCG CTC CCC AAA AAC GAG TTT GAG GCC GGC GGG CTT Pro Leu Tyr Ala Pro Leu Pro Lys Asn Glu Phe Glu Ala Gly Gly Leu 420 425 430	15084
ACG GAC GAT GAG GAA GTG ATT TAT GAC GAA GTA TAC GAA CCC CTA TTT Thr Asp Asp Glu Glu Val Ile Tyr Asp Glu Val Tyr Glu Pro Leu Phe 435 440 445	15132
CGC GGC TAC TGT AAG CAG GAA TTC CGC GAA GAT GTG AAT ACC TTT TTC Arg Gly Tyr Cys Lys Gln Glu Phe Arg Glu Asp Val Asn Thr Phe Phe 450 455 460	15180
GGT GCG GTC GTG GAG GGA GAA AGG GCC TTA AAC TTT AAA TCC GCC ATC Gly Ala Val Val Glu Gly Glu Arg Ala Leu Asn Phe Lys Ser Ala Ile 465 470 475	15228
GCA TCA ATG GCA GAT CGC ATC CTG GCA AAT AAA AGC GGC AGA AGG AAT Ala Ser Met Ala Asp Arg Ile Leu Ala Asn Lys Ser Gly Arg Arg Asn 480 485 490 495	15276
ATG GAT AGC TAT TAG TTGGTC ATG CCT TTT AAG ACC AGA GGG GCC GAA Met Asp Ser Tyr . Met Pro Phe Lys Thr Arg Gly Ala Glu 500 1 5	15324
GAC GCG GCC GCG GGC AAG AAC AGG TTT AAG AAA TCG AGA AAT CGG GAA Asp Ala Ala Ala Gly Lys Asn Arg Phe Lys Lys Ser Arg Asn Arg Glu 10 15 20 25	15372
ATC TTA CCG ACC AGA CTG CGT GGC ACC GGT AAG AAA ACT GCC GGA TTG Ile Leu Pro Thr Arg Leu Arg Gly Thr Gly Lys Lys Thr Ala Gly Leu 30 35 40	15420
TCC AAT TAT ACC CAG CCT ATT CCC TGG AAC CCT AAA TTC TGC AGC GCG Ser Asn Tyr Thr Gln Pro Ile Pro Trp Asn Pro Lys Phe Cys Ser Ala 45 50 55	15468
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Thr Cys Cys Ala Ser Arg Ser Thr Val Ser Ser Gln Pro Asp Ser Pro	
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His Thr Pro Met Pro Thr Glu Tyr Gly Arg Val Pro Ser Ala Lys Arg	
90 95 100 105	
AAA AAA CTA TCA TCT TCA GAC TGC GAG GGC GCG CAC CAA CCC CTA GTA	15660
Lys Lys Leu Ser Ser Ser Asp Cys Glu Gly Ala His Gln Pro Leu Val	
110 115 120	
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Ser Cys Lys Leu Pro Asp Ser Gln Ala Ala Pro Ala Arg Thr Tyr Ser	
125 130 135	
TCT GCG CAA AGA TAT ACT GTT GAC GAG GTT TCG TCG CCA ACT CCG CCA	15756
Ser Ala Gln Arg Tyr Thr Val Asp Glu Val Ser Ser Pro Thr Pro Pro	
140 145 150	
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Gly Val Asp Ala Val Ala Asp Leu Glu Thr Arg Ala Glu Leu Pro Gly	
155 160 165	
GCT ACG ACG GAA CAA ACG GAA AGT AAA AAT AAG CTC CCC AAC CAA CAA	15852
Ala Thr Thr Glu Gln Thr Glu Ser Lys Asn Lys Leu Pro Asn Gln Gln	
170 175 180 185	
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Ser Arg Leu Lys Pro Lys Pro Thr Asn Glu His Val Gly Gly Glu Arg	
190 195 200	
TGC CCC TCC GAA GGC ACG GTC GAG GCG CCA TCG CTC GGC ATC CTC TCG	15948
Cys Pro Ser Glu Gly Thr Val Glu Ala Pro Ser Leu Gly Ile Leu Ser	
205 210 215	
CGC GTC GGG GCA GCG ATA GCA AAC GAG CTG GCT CGT ATG CGG AGG GCG	15996
Arg Val Gly Ala Ala Ile Ala Asn Glu Leu Ala Arg Met Arg Arg Ala	
220 225 230	
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Cys Leu Pro Leu Ala Ala Ser Ala Ala Ala Ala Gly Ile Val Ala Trp	
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Met Ser Lys Cys Tyr	
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Cys Leu Ala Arg His Leu Tyr Lys Ser Pro Arg Cys Val Gly Arg Arg	
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Val Ala Phe Gly Gly Leu Ala Thr Met Ser Arg Pro Pro Thr Ser His	
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Gly Arg Phe Trp Arg Ala Ser Gln Ser Cys Asp Ile Phe Phe Trp Pro	
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GAC CCG CGA ATA GCG CCC GCG GCT AAG CGC GCC GTC GCA GCG GCG GTA Asp Pro Arg Ile Ala Pro Ala Ala Lys Arg Ala Val Ala Ala Val 105 110 115	16479
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GAA ATA AGA GAC GTG CCC AAA GTT CCA GTC ATT GGG CCG GAC ATT CTT Glu Ile Arg Asp Val Pro Lys Val Pro Val Ile Gly Pro Asp Ile Leu 150 155 160 165	16623
TCT TTT TTC TCC GCC GTC GAG CTG CCG GTG CTC TAT ATC AGA GCC Ser Phe Phe Ser Ala Ala Val Glu Leu Pro Val Leu Tyr Ile Arg Ala 170 175 180	16671
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CAC CTC ATG AAC TGT GTA GCT ACC GAT AAG ATC ATG TCT CCG GAC GTG His Leu Met Asn Cys Val Ala Thr Asp Lys Ile Met Ser Pro Asp Val 250 255 260	16911
CGC GTC CCA GTC GAA GAA AGC TTT TAC AGC CAC TGT TTA AGG GAA ATC Arg Val Pro Val Glu Glu Ser Phe Tyr Ser His Cys Leu Arg Glu Ile 265 270 275	16959
ATT ATG TGC GAG AGA GCT TTT TGT TAC CCG TGC AAT CCC CCG CCA AAA Ile Met Cys Glu Arg Ala Phe Cys Tyr Pro Cys Asn Pro Pro Pro Lys 280 285 290	17007
TGG TGA GCTCAGGGTC CCATTTACCC CCGCAACACC CTCTCGCCGC CAGGGCGCGC Trp 295	17063
GCTCTATCTT TCTCTATGTC CCGTCGCCAC CGGCCTAACG GAACGGTGGA ACGGGGCCGC	17123
CCGGGAAAGC CTAGCTCCGC ACAGACACAG ACAGACAAAC GGCCTCTCGA TTGCAACAAC	17183
GTGAAAAACA CACAATAATA TTACTTTATT TATTTTCGCAG CGCTCGCGTG TCGCTCGTTT	17243
CTGGGGGGGG GGGGGGGTTG TGTTTCGCTG CCGCGGAGTG GGTGAGGGGG GAGAGTGGAC	17303

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GGAGGACAGT	GTAAAAACCC	GCGAGGTTGT	CAGGGACGCG	GAGGTAAGGA	AGCCGCTAGA	17363
GGGCGTCATT	CTCCCGTCAA	CGGCGCCGCG	CCAGCGCCAG	CGCGATTCCA	GCGTCCCTCG	17423
CAAAGATCGA	GGCGCTCACT	TCGGGAGAGT	TGGCGGCAGC	CGCGCCGGCG	CGCAAGGCGG	17483
CCAGGTATTG	GCGACGGCGC	ATCTCCGATT	GCGGGACTCT	CCCCGTCCCG	ACGCAGAAAA	17543
GACTCTGCAC	GTAAATCGAG	TCGTACAAAC	ACGCTTCGCG	GCACGGCCGA	GGGTGCCACA	17603
AGCAGCACCA	GTGCCCCGCC	GCCAGGAGAG	ACCGGGAGGT	CTCTCGCTCG	GCGGACGCGA	17663
GGTCGGCCCG	CAGGTGTCGG	GACAGCCAGG	ATAACAGTTC	TTTCTCGATC	ACGAAACGCA	17723
TATTCTCGCT	CTGCATGGTA	CGGCTCTCGT	CCTCGAAGCG	GTCACCGTCC	AGAGAGTCGA	17783
GCCAGAAATC	GCCCTCGATC	CCTTCCATTG	CCTCCTCTAA	TTCTCCCAAC	CCGTTGCCGT	17843
TATTGCGGTC	AGTGGGGGAG	TTGGCGACGC	TCTCCGTCGA	CGCCACCGC	GGCCTCAAAC	17903
CTAGGCCGCG	CGTCGCCCCG	CTGGCCCCCA	GAAAAGCCGA	ACGTAGCCGT	TCGTTGGCAG	17963
CAATCAGCGC	GTTGCGGCGG	TCTCTCGCTG	ACGTGAACTC	TCCGTAACCG	TCCTTGAGTT	18023
CGGACGATAT	CTCGACTAAC	TCGCGCCAGA	GCCGCGAGGC	GATCCGAATG	CACGGGTCTA	18083
CCGAGTCGGC	CGACTCCGAC	GAGGCGACAG	CGGCACCTTG	CCGCCTGCGC	TCGCCACGAG	18143
GTACCGCGTG	CGCAGTAATG	TGATCGCTGT	CCATCAGCGC	CAGCGGGTAG	CACCCGTCGA	18203
GCATGTTTTT	CATTTAGGGA	TGTGTCTAGA	GGAGAGCGGT	CCGGGCGGTC	TACTGCGGTT	18263
GTGCTGGGCC	GAGTTGGACG	GCTACGGATT	GCGCCGGGCG	TGAAGGGGGG	GGGGCGGCGG	18323
GATGTCCGGC	GGTCGCAAAG	GGGCGCGCGT	CCGCTTCTGC	GTGAAGGCTG	AGCGGGAAAG	18383
AAGTTCTGGA	TGAGAAATGA	TCGAGCGGGC	AATAAATGTC	CAGAGTAGGG	GGGTGGGAGG	18443
GAGGGGGAGG	TTCTGCCCCG	CGTCTCCTCT	ATCTGCTCGT	CGAGGCCTCG	GCCTTGCGTC	18503
GCCGTGCAGG	GGTCGAGGCC	GCTTCTTCTT	TTTTACTTCT	CTCCTCGGAT	TCCTCGTCAG	18563
AGGAAGAAGA	AAATGACAAC	CTCCGTCTTT	TAAGAGTGCG	CCTACCCGCC	CTGGCGGCCG	18623
AAGCCTTCCG	TGGGTCTTTG	CGGGTGCCGC	GCACCGCAAT	AACGCACGGA	CGCGGGGGAT	18683
AGCAAATGGC	GGCGGCGCCG	GAGAGCTGTC	GTCAATAAAG	TCTAAGTCAG	ATTGCGTGGG	18743
CTCTGACTCG	GTGGAGCTGT	GTCCCGTGTC	CTCCTCGCCC	AAGTCCACTC	CCCGGCACCC	18803
AGGCTGCTCT	TCCTCCGACT	CCGGGTCGCT	CCAGCTCCTC	CCGCGTGCCG	GTTCTTCGTC	18863
CTCCGATACG	TCCGAAAAGA	AAAACCTTCT	GGAGAGCTCT	TCGGGATCC		18912

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 278 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

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Met	Glu	Asn	Met	Leu	Asp	Gly	Cys	Tyr	Pro	Leu	Ala	Leu	Met	Asp	Ser
1				5					10					15	
Asp	His	Ile	Thr	Ala	His	Ala	Val	Pro	Arg	Gly	Glu	Arg	Arg	Arg	Gln
			20					25					30		
Gly	Ala	Ala	Val	Ala	Ser	Ser	Glu	Ser	Ala	Asp	Ser	Val	Asp	Pro	Cys
	35						40					45			
Ile	Arg	Ile	Ala	Ser	Arg	Leu	Trp	Arg	Glu	Leu	Val	Glu	Ile	Ser	Ser
	50					55					60				
Glu	Leu	Lys	Asp	Gly	Tyr	Gly	Glu	Phe	Thr	Ser	Ala	Arg	Asp	Arg	Arg
65					70					75					80
Asn	Ala	Leu	Ile	Ala	Ala	Asn	Glu	Arg	Leu	Arg	Ser	Ala	Phe	Leu	Gly
				85					90					95	
Ala	Ser	Arg	Ala	Thr	Arg	Gly	Leu	Gly	Leu	Arg	Pro	Arg	Trp	Ala	Ser
			100					105						110	
Thr	Glu	Ser	Val	Ala	Asn	Ser	Pro	Thr	Asp	Pro	Asn	Asn	Gly	Asn	Gly
			115				120						125		
Leu	Gly	Glu	Leu	Glu	Glu	Ala	Met	Glu	Gly	Ile	Glu	Gly	Asp	Phe	Trp
	130					135					140				
Leu	Asp	Ser	Leu	Asp	Gly	Asp	Arg	Phe	Glu	Asp	Glu	Ser	Arg	Thr	Met
145					150					155					160
Gln	Ser	Glu	Asn	Met	Arg	Phe	Val	Ile	Glu	Lys	Glu	Leu	Leu	Ser	Trp
			165						170					175	
Leu	Ser	Arg	His	Leu	Pro	Ala	Asp	Leu	Ala	Ser	Ala	Glu	Arg	Glu	Thr
			180					185					190		
Ser	Arg	Ser	Leu	Leu	Ala	Ala	Gly	His	Trp	Cys	Cys	Leu	Trp	His	Pro
			195				200					205			
Arg	Pro	Cys	Arg	Glu	Ala	Cys	Leu	Tyr	Asp	Ser	Ile	Tyr	Val	Gln	Ser
	210					215					220				
Leu	Phe	Cys	Val	Gly	Thr	Gly	Arg	Val	Pro	Gln	Ser	Glu	Met	Arg	Arg
225					230					235					240
Arg	Glu	Tyr	Leu	Ala	Ala	Leu	Arg	Ala	Gly	Ala	Ala	Ala	Ala	Asn	Ser
				245					250					255	
Pro	Glu	Val	Ser	Ala	Ser	Ile	Phe	Ala	Arg	Asp	Ala	Gly	Ile	Ala	Leu
			260					265					270		
Ala	Leu	Ala	Arg	Arg	Arg										
			275												

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 294 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Met	Ser	Lys	Cys	Tyr	Cys	Leu	Ala	Arg	His	Leu	Tyr	Lys	Ser	Pro	Arg
1				5					10					15	
Cys	Val	Gly	Arg	Arg	Val	Ala	Phe	Gly	Gly	Leu	Ala	Thr	Met	Ser	Arg
			20					25					30		
Pro	Pro	Thr	Ser	His	Leu	Asp	Leu	Ala	Phe	Ser	Ala	Ala	Phe	Arg	Gly
		35				40						45			
Thr	Asp	Leu	Pro	Gly	Gly	Arg	Phe	Trp	Arg	Ala	Ser	Gln	Ser	Cys	Asp
	50					55					60				
Ile	Phe	Phe	Trp	Pro	Asp	Leu	Ala	Ala	Val	Ile	Val	Gln	Ala	Ala	Arg
65					70					75					80
Ala	Tyr	Phe	Glu	Gly	Lys	Glu	Arg	Leu	Gly	Ser	Leu	Gln	Val	Ala	Glu
				85					90					95	
Asp	Ile	Thr	Ala	His	Asp	Pro	Arg	Ile	Ala	Pro	Ala	Ala	Lys	Arg	Ala
			100					105					110		
Val	Ala	Ala	Ala	Val	Gly	Leu	Trp	Thr	Ala	Leu	Ser	Glu	Leu	Val	Gly
			115				120					125			
Gly	Pro	Asn	Gly	Glu	Leu	Glu	Ser	Lys	Val	Trp	Gly	Lys	Gln	Ile	Pro
	130					135					140				
Arg	Ala	Ala	Ala	Trp	Glu	Ile	Arg	Asp	Val	Pro	Lys	Val	Pro	Val	Ile
145					150					155					160
Gly	Pro	Asp	Ile	Leu	Ser	Phe	Phe	Ser	Ala	Ala	Val	Glu	Leu	Pro	Val
				165					170					175	
Leu	Tyr	Ile	Arg	Ala	Arg	Gly	Gly	Ala	His	Ser	Arg	Ser	Ala	His	Trp
			180				185						190		
Asn	Asn	Gln	Ser	Ser	Ala	Pro	Ala	Ala	Gly	Leu	Ala	Ala	Ile	Arg	Ile
		195				200						205			
Gly	Met	Glu	Met	Val	Arg	Ser	Leu	Leu	Val	Ile	Ala	Leu	Pro	Leu	Ser
	210					215					220				
Asn	Phe	Thr	Leu	Pro	Glu	Asp	Leu	Pro	Glu	Gly	Ser	Gln	Asn	Ser	Ile
225					230					235					240
Arg	Ala	Phe	Val	Ala	His	Leu	Met	Asn	Cys	Val	Ala	Thr	Asp	Lys	Ile
				245				250						255	
Met	Ser	Pro	Asp	Val	Arg	Val	Pro	Val	Glu	Glu	Ser	Phe	Tyr	Ser	His
			260				265						270		
Cys	Leu	Arg	Glu	Ile	Ile	Met	Cys	Glu	Arg	Ala	Phe	Cys	Tyr	Pro	Cys
		275					280					285			
Asn	Pro	Pro	Pro	Lys	Trp										
	290														

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 229 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Met	Ala	Pro	Val	Lys	Val	Thr	Ile	Val	Ser	Ala	Val	Asp	Ser	His	Tyr
1				5					10					15	
Lys	Leu	Pro	Asn	Ser	Arg	Phe	Glu	Leu	Ser	Asp	Ser	Gly	Trp	Lys	Glu
			20					25					30		
Leu	Val	His	Ala	Val	Lys	Thr	Met	Ala	Ser	Tyr	Asp	Arg	Pro	Ser	Thr
		35					40					45			
Leu	Ser	Val	Ile	Val	Arg	Pro	Ala	Ser	Leu	Tyr	Glu	Val	Ser	Gly	Glu
	50					55					60				
Leu	Phe	Ser	Leu	Pro	Arg	Met	Cys	Arg	Pro	Val	Ile	Arg	Phe	Gly	Glu
65					70					75					80
Gly	Gly	Asp	Pro	Pro	Gly	Val	Ser	Pro	Glu	Trp	Ser	Gly	Leu	Asp	Ala
				85					90					95	
Gly	Phe	Tyr	His	Leu	Ser	Ser	Gly	Ala	Tyr	Ala	Ala	Lys	Glu	Phe	His
			100					105					110		
Leu	Trp	Val	Leu	Gly	Thr	Ala	Asp	Ile	Cys	Met	Ala	Ala	Leu	Asn	Leu
		115					120						125		
Pro	Ala	Pro	Lys	Thr	Phe	Leu	Ile	Thr	Glu	Thr	Gly	Gly	Lys	Asn	Phe
	130					135					140				
Glu	Arg	Gly	Val	Glu	Ile	Phe	Leu	Val	Asn	Gly	Asp	Lys	Thr	Thr	Leu
145					150					155					160
Ser	Leu	Ser	His	Pro	Ser	Val	Trp	Thr	Thr	Leu	Ala	Pro	Ser	Ser	Leu
				165					170					175	
Arg	Thr	Pro	Trp	Pro	Tyr	Ser	Thr	Val	Lys	Phe	Leu	Lys	Val	Lys	Pro
			180					185					190		
Asn	Ser	Ala	Ala	Tyr	Cys	Val	Ser	Asp	Ser	Asp	Asp	Gly	Glu	Arg	Gln
		195					200					205			
Pro	Lys	Phe	Phe	Leu	Gly	Ser	Leu	Phe	Lys	Ser	Lys	Lys	Pro	Arg	Ser
	210					215					220				
Pro	Arg	Arg	Arg	Arg											
225															

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Met	Arg	Phe	Arg	Arg	Ile	Cys	Ser	Arg	Ser	Arg	Ala	Glu	Lys	Arg	Arg
1				5					10					15	
Arg	Thr	Thr	Glu	Asn	Pro	Leu	Thr	Ser	Lys	Arg	Val	Cys	Val	Leu	Asp
			20					25					30		
Ser	Phe	Ser	Arg	Thr	Met	Ser	Leu	Arg	Pro	Tyr	Ala	Glu	Ile	Leu	Pro
		35					40					45			

Thr	Ala	Glu	Gly	Val	Glu	Arg	Leu	Ala	Glu	Leu	Val	Ser	Val	Thr	Met
50						55					60				
Thr	Glu	Arg	Ala	Glu	Pro	Val	Thr	Glu	Asn	Thr	Ala	Val	Asn	Ser	Ile
65					70					75					80
Pro	Pro	Ala	Asn	Glu	Asn	Gly	Gln	Asn	Phe	Ala	Tyr	Ala	Gly	Asp	Gly
			85					90					95		
Pro	Ser	Thr	Thr	Glu	Lys	Val	Asp	Gly	Ser	His	Thr	Asp	Phe	Asp	Glu
			100					105					110		
Ala	Ser	Ser	Asp	Tyr	Ala	Gly	Pro	Val	Pro	Leu	Ala	Gln	Thr	Arg	Leu
			115				120					125			
Lys	His	Ser	Asp	Glu	Phe	Leu	Gln	His	Phe	Arg	Val	Leu	Asp	Asp	Leu
130						135					140				
Val	Glu	Gly	Ala	Tyr	Gly	Phe	Ile	Cys	Asp	Val	Arg	Arg	Tyr	Thr	Glu
145					150					155					160
Glu	Glu	Gln	Arg	Arg	Arg	Gly	Val	Asn	Ser	Thr	Asn	Gln	Gly	Lys	Ser
			165						170					175	
Lys	Cys	Lys	Arg	Leu	Ile	Ala	Lys	Tyr	Val	Lys	Asn	Gly	Thr	Arg	Ala
			180					185					190		
Ala	Ser	Gln	Leu	Glu	Asn	Glu	Ile	Leu	Val	Leu	Gly	Arg	Leu	Asn	His
			195				200					205			
Glu	Asn	Val	Leu	Lys	Ile	Gln	Glu	Ile	Leu	Arg	Tyr	Pro	Asp	Asn	Thr
210						215					220				
Tyr	Met	Leu	Thr	Gln	Arg	Tyr	Gln	Phe	Asp	Leu	Tyr	Ser	Tyr	Met	Tyr
225					230					235					240
Asp	Glu	Ala	Phe	Asp	Trp	Lys	Asp	Ser	Pro	Met	Leu	Lys	Gln	Thr	Arg
				245					250					255	
Arg	Ile	Met	Lys	Gln	Leu	Met	Ser	Ala	Val	Ser	Tyr	Ile	His	Ser	Lys
			260					265					270		
Lys	Leu	Ile	His	Arg	Asp	Ile	Lys	Leu	Glu	Asn	Ile	Phe	Leu	Asn	Cys
			275				280					285			
Asp	Gly	Lys	Thr	Val	Leu	Gly	Asp	Phe	Gly	Thr	Val	Thr	Pro	Phe	Glu
290						295					300				
Asn	Glu	Arg	Glu	Pro	Phe	Glu	Tyr	Gly	Trp	Val	Gly	Thr	Val	Ala	Thr
305					310					315					320
Asn	Ser	Pro	Glu	Ile	Leu	Ala	Arg	Asp	Ser	Tyr	Cys	Glu	Ile	Thr	Asp
			325						330					335	
Ile	Trp	Ser	Cys	Gly	Val	Val	Leu	Leu	Glu	Met	Val	Ser	His	Glu	Phe
			340					345					350		
Cys	Pro	Ile	Gly	Asp	Gly	Gly	Gly	Asn	Pro	His	Gln	Gln	Leu	Leu	Lys
			355				360					365			
Val	Ile	Asp	Ser	Leu	Ser	Val	Cys	Asp	Glu	Glu	Phe	Pro	Asp	Pro	Pro
			370			375					380				
Cys	Asn	Leu	Tyr	Asn	Tyr	Leu	His	Tyr	Ala	Ser	Ile	Asp	Arg	Ala	Gly
385					390					395					400

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(2) INFORMATION FOR SEQ ID NO:64:

(A) LENGTH: 623 amino acids

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Met 1	Thr	Leu	Pro	His 5	Arg	Leu	Thr	Lys	Arg 10	Pro	Phe	Ala	Arg	Arg 15	Phe
Cys	Ser	Val	Phe 20	Val	Ile	His	Tyr	Ser 25	Glu	Thr	Lys	Leu	Asp 30	Arg	Tyr
Asn	Lys	Thr 35	Met	Leu	Leu	Tyr	Arg 40	Pro	Asp	Ser	Thr	Met 45	Arg	His	Ser
Gly 50	Gly	Asp	Ala	Asn	His	Arg 55	Gly	Ile	Arg	Pro	Arg 60	Arg	Lys	Ser	Ile
Gly 65	Ala	Phe	Ser	Ala	Arg 70	Glu	Lys	Thr	Gly	Lys 75	Arg	Asn	Ala	Leu	Thr 80
Glu	Ser	Ser	Ser	Ser 85	Ser	Asp	Met	Leu	Asp 90	Pro	Phe	Ser	Thr	Asp 95	Lys
Glu	Phe	Gly	Gly 100	Lys	Trp	Thr	Val	Asp 105	Gly	Pro	Ala	Asp	Ile 110	Thr	Ala
Glu	Val	Leu 115	Ser	Gln	Ala	Trp	Asp 120	Val	Leu	Gln	Leu	Val 125	Lys	His	Glu
Asp 130	Ala	Glu	Glu	Glu	Arg	Val 135	Thr	Tyr	Glu	Ser	Lys 140	Pro	Thr	Pro	Ile
Gln 145	Pro	Phe	Asn	Ala	Trp 150	Pro	Asp	Gly	Pro	Ser 155	Trp	Asn	Ala	Gln	Asp 160
Phe	Thr	Arg	Ala	Pro 165	Ile	Val	Tyr	Pro	Ser 170	Ala	Glu	Val	Leu	Asp 175	Ala
Glu	Ala	Leu	Lys 180	Val	Gly	Ala	Phe	Val 185	Ser	Arg	Val	Leu	Gln 190	Cys	Val
Pro	Phe	Thr 195	Arg	Ser	Lys	Lys	Ser 200	Val	Thr	Val	Arg	Asp 205	Ala	Gln	Ser

Ile Ser Asp His Ala Arg Glu Ile Ile Ala Asp Gly Val Arg Phe Lys
565 570 575
Pro Val Ile Asp Glu Pro Val Arg Ala Ser Val Ala Leu Ser Thr Ala
580 585 590
Ala Ala Gly Lys Val Lys Ala Arg Arg Leu Thr Ser Val Arg Ala Pro
595 600 605
Val Pro Gly Ala Gly Ala Val Ser Ala Arg Arg Lys Ser Glu Ile
610 615 620

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 292 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Met Ser Gly Phe Ser Asn Ile Gly Ser Ile Ala Thr Val Ser Leu Val
1 5 10 15
Cys Ser Leu Leu Cys Ala Ser Val Leu Gly Ala Pro Val Leu Asp Gly
20 25 30
Leu Glu Ser Ser Pro Phe Pro Phe Gly Gly Lys Ile Ile Ala Gln Ala
35 40 45
Cys Asn Arg Thr Thr Ile Glu Val Thr Val Pro Trp Ser Asp Tyr Ser
50 55 60
Gly Arg Thr Glu Gly Val Ser Val Glu Val Lys Trp Phe Tyr Gly Asn
65 70 75 80
Ser Asn Pro Glu Ser Phe Val Phe Gly Val Asp Ser Glu Thr Gly Ser
85 90 95
Gly His Glu Asp Leu Ser Thr Cys Trp Ala Leu Ile His Asn Leu Asn
100 105 110
Ala Ser Val Cys Arg Ala Ser Asp Ala Gly Ile Pro Asp Phe Asp Lys
115 120 125
Gln Cys Glu Lys Val Gln Arg Arg Leu Arg Ser Gly Val Glu Leu Gly
130 135 140
Ser Tyr Val Ser Gly Asn Gly Ser Leu Val Leu Tyr Pro Gly Met Tyr
145 150 155 160
Asp Ala Gly Ile Tyr Ala Tyr Gln Leu Ser Val Gly Gly Lys Gly Tyr
165 170 175
Thr Gly Ser Val Tyr Leu Asp Val Gly Pro Asn Pro Gly Cys His Asp
180 185 190
Gln Tyr Gly Tyr Thr Tyr Tyr Ser Leu Ala Asp Glu Ala Ser Asp Leu
195 200 205
Ser Ser Tyr Asp Val Ala Ser Pro Glu Leu Asp Gly Pro Met Glu Glu
210 215 220

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Asp Tyr Ser Asn Cys Leu Asp Met Pro Pro Leu Arg Pro Trp Thr Thr
 225 230 235 240
 Val Cys Ser His Asp Val Glu Glu Gln Glu Asn Ala Thr Asp Glu Leu
 245 250 255
 Tyr Leu Trp Asp Glu Glu Cys Ala Gly Pro Leu Asp Glu Tyr Val Asp
 260 265 270
 Glu Arg Ser Glu Thr Met Pro Arg Met Val Val Phe Ser Pro Pro Ser
 275 280 285
 Thr Leu Gln Gln .
 290

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 985 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Met Gly Thr Met Leu Val Leu Arg Leu Phe Leu Leu Ala Val Ala Asp
 1 5 10 15
 Ala Ala Leu Pro Thr Gly Arg Phe Cys Arg Val Trp Lys Val Pro Pro
 20 25 30
 Gly Gly Thr Ile Gln Glu Asn Leu Ala Val Leu Ala Glu Ser Pro Val
 35 40 45
 Thr Gly His Ala Thr Tyr Pro Pro Pro Glu Gly Ala Val Ser Phe Gln
 50 55 60
 Ile Phe Ala Asp Thr Pro Thr Leu Arg Ile Arg Tyr Gly Ala Thr Glu
 65 70 75 80
 Asp Glu Leu Ala Leu Glu Arg Gly Thr Ser Ala Ser Asp Ala Asp Asn
 85 90 95
 Val Thr Phe Ser Leu Ser Tyr Arg Pro Arg Pro Glu Ile His Gly Ala
 100 105 110
 Tyr Phe Thr Ile Gly Val Phe Ala Thr Gly Gln Ser Thr Glu Ser Ser
 115 120 125
 Tyr Ser Val Ile Ser Arg Val Leu Val Asn Ala Ser Leu Glu Arg Ser
 130 135 140
 Val Arg Leu Glu Thr Pro Cys Asp Glu Asn Phe Leu Gln Asn Glu Pro
 145 150 155 160
 Thr Trp Gly Ser Lys Arg Trp Leu Gly Pro Pro Ser Pro Tyr Val Arg
 165 170 175
 Asp Asn Asp Val Ala Val Leu Thr Lys Ala Gln Tyr Ile Gly Glu Cys
 180 185 190
 Tyr Ser Asn Ser Ala Ala Gln Thr Gly Leu Thr Ser Leu Asn Met Thr
 195 200 205

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Phe	Phe	Tyr	Ser	Pro	Lys	Arg	Ile	Val	Asn	Val	Thr	Trp	Thr	Thr	Gly
210						215					220				
Gly	Pro	Ser	Pro	Ser	Arg	Ile	Thr	Val	Tyr	Ser	Ser	Arg	Glu	Asn	Gly
225					230					235					240
Gln	Pro	Val	Leu	Arg	Asn	Val	Ser	Asp	Gly	Phe	Leu	Val	Lys	Tyr	Thr
				245					250					255	
Pro	Asp	Ile	Asp	Gly	Arg	Ala	Met	Ile	Asn	Val	Ile	Ala	Asn	Tyr	Ser
			260					265					270		
Pro	Ala	Asp	Ser	Gly	Ser	Val	Leu	Ala	Phe	Thr	Ala	Phe	Arg	Glu	Gly
		275					280					285			
Lys	Leu	Pro	Ser	Ala	Ile	Gln	Leu	His	Arg	Ile	Asp	Met	Ser	Gly	Thr
290						295					300				
Glu	Pro	Pro	Gly	Thr	Glu	Thr	Thr	Phe	Asp	Cys	Gln	Lys	Met	Ile	Glu
305					310					315					320
Thr	Pro	Tyr	Arg	Ala	Leu	Gly	Ser	Asn	Val	Pro	Arg	Asp	Asp	Ser	Ile
				325					330					335	
Arg	Pro	Gly	Ala	Thr	Leu	Pro	Pro	Phe	Asp	Thr	Ala	Ala	Pro	Asp	Phe
			340					345					350		
Asp	Thr	Gly	Thr	Ser	Pro	Thr	Pro	Thr	Thr	Val	Pro	Glu	Pro	Ala	Ile
		355					360					365			
Thr	Thr	Leu	Ile	Pro	Arg	Ser	Thr	Ser	Asp	Met	Gly	Phe	Phe	Ser	Thr
370						375					380				
Ala	Arg	Ala	Thr	Gly	Ser	Glu	Thr	Leu	Ser	Val	Pro	Val	Gln	Glu	Thr
385					390					395					400
Asp	Arg	Thr	Leu	Ser	Thr	Thr	Pro	Leu	Thr	Leu	Pro	Leu	Thr	Pro	Gly
				405				410						415	
Glu	Ser	Glu	Asn	Thr	Leu	Phe	Pro	Thr	Thr	Ala	Pro	Gly	Ile	Ser	Thr
			420					425					430		
Glu	Thr	Pro	Ser	Ala	Ala	His	Glu	Thr	Thr	Gln	Thr	Gln	Ser	Ala	Glu
		435					440					445			
Thr	Val	Val	Phe	Thr	Gln	Ser	Pro	Ser	Thr	Glu	Ser	Glu	Thr	Ala	Arg
	450					455					460				
Ser	Gln	Ser	Gln	Glu	Pro	Trp	Tyr	Phe	Thr	Gln	Thr	Pro	Ser	Thr	Glu
465					470					475					480
Gln	Ala	Ala	Leu	Thr	Gln	Thr	Gln	Ile	Ala	Glu	Thr	Glu	Ala	Leu	Phe
				485					490					495	
Thr	Gln	Thr	Pro	Ser	Ala	Glu	Gln	Met	Thr	Phe	Thr	Gln	Thr	Pro	Gly
			500					505					510		
Ala	Glu	Thr	Glu	Ala	Pro	Ala	Gln	Thr	Pro	Ser	Thr	Ile	Pro	Glu	Ile
		515					520					525			
Phe	Thr	Gln	Ser	Arg	Ser	Thr	Pro	Pro	Glu	Thr	Ala	Arg	Ala	Pro	Ser
	530					535					540				
Ala	Ala	Pro	Glu	Val	Phe	Thr	Gln	Ser	Ser	Ser	Thr	Val	Thr	Glu	Val
545					550					555					560

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Phe	Thr	Gln	Thr	Pro 565	Ser	Thr	Val	Pro	Lys 570	Thr	Thr	Leu	Ser	Ser 575	Ser
Thr	Glu	Pro	Ala 580	Ile	Phe	Thr	Arg	Thr 585	Gln	Ser	Ala	Gly	Thr 590	Glu	Ala
Phe	Thr	Gln 595	Thr	Ser	Ser	Ala	Glu 600	Pro	Asp	Thr	Met	Arg 605	Thr	Gln	Ser
Thr	Glu 610	Thr	His	Phe	Phe	Thr 615	Gln	Ala	Pro	Ser	Thr 620	Val	Pro	Lys	Ala
Thr 625	Gln	Thr	Pro	Ser	Thr 630	Glu	Pro	Glu	Val	Leu 635	Thr	Gln	Ser	Pro	Ser 640
Thr	Glu	Pro	Val 645	Pro	Phe	Thr	Arg	Thr	Leu 650	Gly	Ala	Glu	Pro	Glu 655	Ile
Thr	Gln	Thr	Pro 660	Ser	Ala	Ala	Pro	Glu 665	Val	Tyr	Thr	Arg	Ser 670	Ser	Ser
Thr	Met	Pro 675	Glu	Thr	Ala	Gln	Ser 680	Thr	Pro	Leu	Ala	Ser 685	Gln	Asn	Pro
Thr	Ser 690	Ser	Gly	Thr	Gly 695	Thr	His	Asn	Thr	Glu	Pro 700	Arg	Thr	Tyr	Pro
Val 705	Gln	Thr	Thr	Pro	His 710	Thr	Gln	Lys	Leu	Tyr 715	Thr	Glu	Asn	Lys	Thr 720
Leu	Ser	Phe	Pro 725	Thr	Val	Val	Ser	Glu	Phe 730	His	Glu	Met	Ser	Thr 735	Ala
Glu	Ser	Gln 740	Thr	Pro	Leu	Leu	Asp 745	Val	Lys	Ile	Val	Glu	Val 750	Lys	Phe
Ser	Asn	Asp 755	Gly	Glu	Val	Thr	Ala 760	Thr	Cys	Val	Ser	Thr 765	Val	Lys	Ser
Pro	Tyr 770	Arg	Val	Glu	Thr	Asn 775	Trp	Lys	Val	Asp	Leu 780	Val	Asp	Val	Met
Asp 785	Glu	Ile	Ser	Gly	Asn 790	Ser	Pro	Ala	Gly	Val 795	Phe	Asn	Ser	Asn	Glu 800
Lys	Trp	Gln	Lys 805	Gln	Leu	Tyr	Tyr	Arg	Val 810	Thr	Asp	Gly	Arg	Thr 815	Ser
Val	Gln	Leu 820	Met	Cys	Leu	Ser	Cys 825	Thr	Ser	His	Ser	Pro	Glu 830	Pro	Tyr
Cys	Leu 835	Phe	Asp	Thr	Ser	Leu	Ile 840	Ala	Arg	Glu	Lys	Asp 845	Ile	Ala	Pro
Glu 850	Leu	Tyr	Phe	Thr	Ser	Asp 855	Pro	Gln	Thr	Ala	Tyr 860	Cys	Thr	Ile	Thr
Leu 865	Pro	Ser	Gly	Val	Val 870	Pro	Arg	Phe	Glu	Trp 875	Ser	Leu	Asn	Asn	Val 880
Ser	Leu	Pro	Glu 885	Tyr	Leu	Thr	Ala	Thr	Thr 890	Val	Val	Ser	His	Thr 895	Ala
Gly	Gln	Ser	Thr 900	Val	Trp	Lys	Ser	Ser 905	Ala	Arg	Ala	Gly	Glu 910	Ala	Trp

Ile Ser Gly Arg Gly Gly Asn Ile Tyr Glu Cys Thr Val Leu Ile Ser
 915 920 925
 Asp Gly Thr Arg Val Thr Thr Arg Lys Glu Arg Cys Leu Thr Asn Thr
 930 935 940
 Trp Ile Ala Val Glu Asn Gly Ala Ala Gln Ala Gln Leu Tyr Ser Leu
 945 950 955 960
 Phe Ser Gly Leu Val Ser Gly Leu Cys Gly Ser Ile Ser Ala Leu Tyr
 965 970 975
 Ala Thr Leu Trp Thr Ala Ile Tyr Phe .
 980 985

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 434 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Met His Arg Pro His Leu Arg Arg His Ser Arg Tyr Tyr Ala Lys Gly
 1 5 10 15
 Glu Val Leu Asn Lys His Met Asp Cys Gly Gly Lys Arg Cys Cys Ser
 20 25 30
 Gly Ala Ala Val Phe Thr Leu Phe Trp Thr Cys Val Arg Ile Met Arg
 35 40 45
 Glu His Ile Cys Phe Val Arg Asn Ala Met Asp Arg His Leu Phe Leu
 50 55 60
 Arg Asn Ala Phe Trp Thr Ile Val Leu Leu Ser Ser Phe Ala Ser Gln
 65 70 75 80
 Ser Thr Ala Ala Val Thr Tyr Asp Tyr Ile Leu Gly Arg Arg Ala Leu
 85 90 95
 Asp Ala Leu Thr Ile Pro Ala Val Gly Pro Tyr Asn Arg Tyr Leu Thr
 100 105 110
 Arg Val Ser Arg Gly Cys Asp Val Val Glu Leu Asn Pro Ile Ser Asn
 115 120 125
 Val Asp Asp Met Ile Ser Ala Ala Lys Glu Lys Glu Lys Gly Gly Pro
 130 135 140
 Phe Glu Ala Ser Val Val Trp Phe Tyr Val Ile Lys Gly Asp Asp Gly
 145 150 155 160
 Glu Asp Lys Tyr Cys Pro Ile Tyr Arg Lys Glu Tyr Arg Glu Cys Gly
 165 170 175
 Asp Val Gln Leu Leu Ser Glu Cys Ala Val Gln Ser Ala Gln Met Trp
 180 185 190
 Ala Val Asp Tyr Val Pro Ser Thr Leu Val Ser Arg Asn Gly Ala Gly
 195 200 205

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Leu Thr Ile Phe Ser Pro Thr Ala Ala Leu Ser Gly Gln Tyr Leu Leu
210 215 220

Thr Leu Lys Ile Gly Arg Phe Ala Gln Thr Ala Leu Val Thr Leu Glu
225 230 235 240

Val Asn Asp Arg Cys Leu Lys Ile Gly Ser Gln Leu Asn Phe Leu Pro
245 250 255

Ser Lys Cys Trp Thr Thr Glu Gln Tyr Gln Thr Gly Phe Gln Gly Glu
260 265 270

His Leu Tyr Pro Ile Ala Asp Thr Asn Thr Arg His Ala Asp Asp Val
275 280 285

Tyr Arg Gly Tyr Glu Asp Ile Leu Gln Arg Trp Asn Asn Leu Leu Arg
290 295 300

Lys Lys Asn Pro Ser Ala Pro Asp Pro Arg Pro Asp Ser Val Pro Gln
305 310 315 320

Glu Ile Pro Ala Val Thr Lys Lys Ala Glu Gly Arg Thr Pro Asp Ala
325 330 335

Glu Ser Ser Glu Lys Lys Ala Pro Pro Glu Asp Ser Glu Asp Asp Met
340 345 350

Gln Ala Glu Ala Ser Gly Glu Asn Pro Ala Ala Leu Pro Glu Asp Asp
355 360 365

Glu Val Pro Glu Asp Thr Glu His Asp Asp Pro Asn Ser Asp Pro Asp
370 375 380

Tyr Tyr Asn Asp Met Pro Ala Val Ile Pro Val Glu Glu Thr Thr Lys
385 390 395 400

Ser Ser Asn Ala Val Ser Met Pro Ile Phe Ala Ala Phe Val Ala Cys
405 410 415

Ala Val Ala Leu Val Gly Leu Leu Val Trp Ser Ile Val Lys Cys Ala
420 425 430

Arg Ser .

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 362 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Met Ala Ser Leu Leu Gly Thr Leu Ala Leu Leu Ala Ala Thr Leu Ala
1 5 10 15

Pro Phe Gly Ala Met Gly Ile Val Ile Thr Gly Asn His Val Ser Ala
20 25 30

Arg Ile Asp Asp Asp His Ile Val Ile Val Ala Pro Arg Pro Glu Ala
35 40 45

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Thr Ile Gln Leu Gln Leu Phe Phe Met Pro Gly Gln Arg Pro His Lys
50 55 60

Pro Tyr Ser Gly Thr Val Arg Val Ala Phe Arg Ser Asp Ile Thr Asn
65 70 75 80

Gln Cys Tyr Gln Glu Leu Ser Glu Glu Arg Phe Glu Asn Cys Thr His
85 90 95

Arg Ser Ser Ser Val Phe Val Gly Cys Lys Val Thr Glu Tyr Thr Phe
100 105 110

Ser Ala Ser Asn Arg Leu Thr Gly Pro Pro His Pro Phe Lys Leu Thr
115 120 125

Ile Arg Asn Pro Arg Pro Asn Asp Ser Gly Met Phe Tyr Val Ile Val
130 135 140

Arg Leu Asp Asp Thr Lys Glu Pro Ile Asp Val Phe Ala Ile Gln Leu
145 150 155 160

Ser Val Tyr Gln Phe Ala Asn Thr Ala Ala Thr Arg Gly Leu Tyr Ser
165 170 175

Lys Ala Ser Cys Arg Thr Phe Gly Leu Pro Thr Val Gln Leu Glu Ala
180 185 190

Tyr Leu Arg Thr Glu Glu Ser Trp Arg Asn Trp Gln Ala Tyr Val Ala
195 200 205

Thr Glu Ala Thr Thr Thr Ser Ala Glu Ala Thr Thr Pro Thr Pro Val
210 215 220

Thr Ala Thr Ser Ala Ser Glu Leu Glu Ala Glu His Phe Thr Phe Pro
225 230 235 240

Trp Leu Glu Asn Gly Val Asp His Tyr Glu Pro Thr Pro Ala Asn Glu
245 250 255

Asn Ser Asn Val Thr Val Arg Leu Gly Thr Met Ser Pro Thr Leu Ile
260 265 270

Gly Val Thr Val Ala Ala Val Val Ser Ala Thr Ile Gly Leu Val Ile
275 280 285

Val Ile Ser Ile Val Thr Arg Asn Met Cys Thr Pro His Arg Lys Leu
290 295 300

Asp Thr Val Ser Gln Asp Asp Glu Glu Arg Ser Gln Thr Arg Arg Glu
305 310 315 320

Ser Arg Lys Phe Gly Pro Met Val Ala Cys Glu Ile Asn Lys Gly Ala
325 330 335

Asp Gln Asp Ser Glu Leu Val Glu Leu Val Ala Ile Val Asn Pro Ser
340 345 350

Ala Leu Ser Ser Pro Asp Ser Ile Lys Met .
355 360

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 499 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Met	Asn	Met	Leu	Val	Ile	Val	Leu	Ala	Ser	Cys	Leu	Ala	Arg	Leu	Thr	1	5	10	15
Phe	Ala	Thr	Arg	His	Val	Leu	Phe	Leu	Glu	Gly	Thr	Gln	Ala	Val	Leu	20	25	30	
Gly	Glu	Asp	Asp	Pro	Arg	Asn	Val	Pro	Glu	Gly	Thr	Val	Ile	Lys	Trp	35	40	45	
Thr	Lys	Val	Leu	Arg	Asn	Ala	Cys	Lys	Met	Lys	Ala	Ala	Asp	Val	Cys	50	55	60	
Ser	Ser	Pro	Asn	Tyr	Cys	Phe	His	Asp	Leu	Ile	Tyr	Asp	Gly	Gly	Lys	65	70	75	80
Lys	Asp	Cys	Pro	Pro	Ala	Gly	Pro	Leu	Ser	Ala	Asn	Leu	Val	Ile	Leu	85	90	95	
Leu	Lys	Arg	Gly	Glu	Ser	Phe	Val	Val	Leu	Gly	Ser	Gly	Leu	His	Asn	100	105	110	
Ser	Asn	Ile	Thr	Asn	Ile	Met	Trp	Thr	Glu	Tyr	Gly	Gly	Leu	Leu	Phe	115	120	125	
Asp	Pro	Val	Thr	Arg	Ser	Asp	Glu	Gly	Ile	Tyr	Phe	Arg	Arg	Ile	Ser	130	135	140	
Gln	Pro	Asp	Leu	Ala	Met	Glu	Thr	Thr	Ser	Tyr	Asn	Val	Ser	Val	Leu	145	150	155	160
Ser	His	Val	Asp	Glu	Lys	Ala	Pro	Ala	Pro	His	Glu	Val	Glu	Ile	Asp	165	170	175	
Thr	Ile	Lys	Pro	Ser	Glu	Ala	His	Ala	His	Val	Glu	Leu	Gln	Met	Leu	180	185	190	
Pro	Phe	His	Glu	Leu	Asn	Asp	Asn	Ser	Pro	Thr	Tyr	Val	Thr	Pro	Val	195	200	205	
Leu	Arg	Val	Phe	Pro	Pro	Thr	Glu	His	Val	Lys	Phe	Asn	Val	Thr	Tyr	210	215	220	
Ser	Trp	Tyr	Gly	Phe	Asp	Val	Lys	Glu	Glu	Cys	Glu	Glu	Val	Lys	Leu	225	230	235	240
Phe	Glu	Pro	Cys	Val	Tyr	His	Pro	Thr	Asp	Gly	Lys	Cys	Gln	Phe	Pro	245	250	255	
Ala	Thr	Asn	Gln	Arg	Cys	Leu	Ile	Gly	Ser	Val	Leu	Met	Ala	Glu	Phe	260	265	270	
Leu	Gly	Ala	Ala	Ser	Leu	Leu	Asp	Cys	Ser	Arg	Asp	Thr	Leu	Glu	Asp	275	280	285	
Cys	His	Glu	Asn	Arg	Val	Pro	Asn	Leu	Arg	Phe	Asp	Ser	Arg	Leu	Ser	290	295	300	
Glu	Ser	Arg	Ala	Gly	Leu	Val	Ile	Ser	Pro	Leu	Ile	Ala	Ile	Pro	Lys	305	310	315	320
Val	Leu	Ile	Ile	Val	Val	Ser	Asp	Gly	Asp	Ile	Leu	Gly	Trp	Ser	Tyr	325	330	335	

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Thr Val Leu Gly Lys Arg Asn Ser Pro Arg Val Val Val Glu Thr His
340 345 350
Met Pro Ser Lys Val Pro Met Asn Lys Val Val Ile Gly Ser Pro Gly
355 360 365
Pro Met Asp Glu Thr Gly Asn Tyr Lys Met Tyr Phe Val Val Ala Gly
370 375 380
Val Ala Ala Thr Cys Val Ile Leu Thr Cys Ala Leu Leu Val Gly Lys
385 390 395 400
Lys Lys Cys Pro Ala His Gln Met Gly Thr Phe Ser Lys Thr Glu Pro
405 410 415
Leu Tyr Ala Pro Leu Pro Lys Asn Glu Phe Glu Ala Gly Gly Leu Thr
420 425 430
Asp Asp Glu Glu Val Ile Tyr Asp Glu Val Tyr Glu Pro Leu Phe Arg
435 440 445
Gly Tyr Cys Lys Gln Glu Phe Arg Glu Asp Val Asn Thr Phe Phe Gly
450 455 460
Ala Val Val Glu Gly Glu Arg Ala Leu Asn Phe Lys Ser Ala Ile Ala
465 470 475 480
Ser Met Ala Asp Arg Ile Leu Ala Asn Lys Ser Gly Arg Arg Asn Met
485 490 495
Asp Ser Tyr .

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 260 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Met Pro Phe Lys Thr Arg Gly Ala Glu Asp Ala Ala Ala Gly Lys Asn
1 5 10 15
Arg Phe Lys Lys Ser Arg Asn Arg Glu Ile Leu Pro Thr Arg Leu Arg
20 25 30
Gly Thr Gly Lys Lys Thr Ala Gly Leu Ser Asn Tyr Thr Gln Pro Ile
35 40 45
Pro Trp Asn Pro Lys Phe Cys Ser Ala Arg Gly Glu Ser Asp Asn His
50 55 60
Ala Cys Lys Asp Thr Phe Tyr Arg Arg Thr Cys Cys Ala Ser Arg Ser
65 70 75 80
Thr Val Ser Ser Gln Pro Asp Ser Pro His Thr Pro Met Pro Thr Glu
85 90 95
Tyr Gly Arg Val Pro Ser Ala Lys Arg Lys Lys Leu Ser Ser Ser Asp
100 105 110

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Cys Glu Gly Ala His Gln Pro Leu Val Ser Cys Lys Leu Pro Asp Ser
115 120 125
Gln Ala Ala Pro Ala Arg Thr Tyr Ser Ser Ala Gln Arg Tyr Thr Val
130 135 140
Asp Glu Val Ser Ser Pro Thr Pro Pro Gly Val Asp Ala Val Ala Asp
145 150 155 160
Leu Glu Thr Arg Ala Glu Leu Pro Gly Ala Thr Thr Glu Gln Thr Glu
165 170 175
Ser Lys Asn Lys Leu Pro Asn Gln Gln Ser Arg Leu Lys Pro Lys Pro
180 185 190
Thr Asn Glu His Val Gly Gly Glu Arg Cys Pro Ser Glu Gly Thr Val
195 200 205
Glu Ala Pro Ser Leu Gly Ile Leu Ser Arg Val Gly Ala Ala Ile Ala
210 215 220
Asn Glu Leu Ala Arg Met Arg Arg Ala Cys Leu Pro Leu Ala Ala Ser
225 230 235 240
Ala Ala Ala Ala Gly Ile Val Ala Trp Ala Ala Arg Ala Leu Gln
245 250 255
Lys Gln Gly Arg .
260

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 294 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Met Ser Lys Cys Tyr Cys Leu Ala Arg His Leu Tyr Lys Ser Pro Arg
1 5 10 15
Cys Val Gly Arg Arg Val Ala Phe Gly Gly Leu Ala Thr Met Ser Arg
20 25 30
Pro Pro Thr Ser His Leu Asp Leu Ala Phe Ser Ala Ala Phe Arg Gly
35 40 45
Thr Asp Leu Pro Gly Gly Arg Phe Trp Arg Ala Ser Gln Ser Cys Asp
50 55 60
Ile Phe Phe Trp Pro Asp Leu Ala Ala Val Ile Val Gln Ala Ala Arg
65 70 75 80
Ala Tyr Phe Glu Gly Lys Glu Arg Leu Gly Ser Leu Gln Val Ala Glu
85 90 95
Asp Ile Thr Ala His Asp Pro Arg Ile Ala Pro Ala Ala Lys Arg Ala
100 105 110
Val Ala Ala Ala Val Gly Leu Trp Thr Ala Leu Ser Glu Leu Val Gly
115 120 125

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Gly Pro Asn Gly Glu Leu Glu Ser Lys Val Trp Gly Lys Gln Ile Pro
130 135 140

Arg Ala Ala Ala Trp Glu Ile Arg Asp Val Pro Lys Val Pro Val Ile
145 150 155 160

Gly Pro Asp Ile Leu Ser Phe Phe Ser Ala Ala Val Glu Leu Pro Val
165 170 175

Leu Tyr Ile Arg Ala Arg Gly Gly Ala His Ser Arg Ser Ala His Trp
180 185 190

Asn Asn Gln Ser Ser Ala Pro Ala Ala Gly Leu Ala Ala Ile Arg Ile
195 200 205

Gly Met Glu Met Val Arg Ser Leu Leu Val Ile Ala Leu Pro Leu Ser
210 215 220

Asn Phe Thr Leu Pro Glu Asp Leu Pro Glu Gly Ser Gln Asn Ser Ile
225 230 235 240

Arg Ala Phe Val Ala His Leu Met Asn Cys Val Ala Thr Asp Lys Ile
245 250 255

Met Ser Pro Asp Val Arg Val Pro Val Glu Glu Ser Phe Tyr Ser His
260 265 270

Cys Leu Arg Glu Ile Ile Met Cys Glu Arg Ala Phe Cys Tyr Pro Cys
275 280 285

Asn Pro Pro Pro Lys Trp .
290

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 278 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Met Glu Asn Met Leu Asp Gly Cys Tyr Pro Leu Ala Leu Met Asp Ser
1 5 10 15

Asp His Ile Thr Ala His Ala Val Pro Arg Gly Glu Arg Arg Arg Gln
20 25 30

Gly Ala Ala Val Ala Ser Ser Glu Ser Ala Asp Ser Val Asp Pro Cys
35 40 45

Ile Arg Ile Ala Ser Arg Leu Trp Arg Glu Leu Val Glu Ile Ser Ser
50 55 60

Glu Leu Lys Asp Gly Tyr Gly Glu Phe Thr Ser Ala Arg Asp Arg Arg
65 70 75 80

Asn Ala Leu Ile Ala Ala Asn Glu Arg Leu Arg Ser Ala Phe Leu Gly
85 90 95

Ala Ser Arg Ala Thr Arg Gly Leu Gly Leu Arg Pro Arg Trp Ala Ser
100 105 110

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Thr	Glu	Ser	Val	Ala	Asn	Ser	Pro	Thr	Asp	Pro	Asn	Asn	Gly	Asn	Gly
	115						120					125			
Leu	Gly	Glu	Leu	Glu	Glu	Ala	Met	Glu	Gly	Ile	Glu	Gly	Asp	Phe	Trp
	130					135					140				
Leu	Asp	Ser	Leu	Asp	Gly	Asp	Arg	Phe	Glu	Asp	Glu	Ser	Arg	Thr	Met
145					150					155					160
Gln	Ser	Glu	Asn	Met	Arg	Phe	Val	Ile	Glu	Lys	Glu	Leu	Leu	Ser	Trp
				165					170					175	
Leu	Ser	Arg	His	Leu	Pro	Ala	Asp	Leu	Ala	Ser	Ala	Glu	Arg	Glu	Thr
			180					185					190		
Ser	Arg	Ser	Leu	Leu	Ala	Ala	Gly	His	Trp	Cys	Cys	Leu	Trp	His	Pro
	195						200					205			
Arg	Pro	Cys	Arg	Glu	Ala	Cys	Leu	Tyr	Asp	Ser	Ile	Tyr	Val	Gln	Ser
	210					215					220				
Leu	Phe	Cys	Val	Gly	Thr	Gly	Arg	Val	Pro	Gln	Ser	Glu	Met	Arg	Arg
225					230					235					240
Arg	Glu	Tyr	Leu	Ala	Ala	Leu	Arg	Ala	Gly	Ala	Ala	Ala	Ala	Asn	Ser
				245					250					255	
Pro	Glu	Val	Ser	Ala	Ser	Ile	Phe	Ala	Arg	Asp	Ala	Gly	Ile	Ala	Leu
				260				265					270		
Ala	Leu	Ala	Arg	Arg	Arg										
		275													

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